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☐ **1:** NM_005191. Homo sapiens CD80...[gi:31377790]   Links

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LOCUS       NM_005191               2824 bp    mRNA    linear   PRI 22-DEC-2003
DEFINITION  Homo sapiens CD80 antigen (CD28 antigen ligand 1, B7-1 antigen)
            (CD80), mRNA.
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VERSION     NM_005191.2  GI:31377790
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2824)
  AUTHORS   Clayton,A.R., Prue,R.L., Harper,L., Drayson,M.T. and Savage,C.O.
  TITLE     Dendritic cell uptake of human apoptotic and necrotic neutrophils
            inhibits CD40, CD80, and CD86 expression and reduces allogeneic T
            cell responses: relevance to systemic vasculitis
  JOURNAL   Arthritis Rheum. 48 (8), 2362-2374 (2003)
   PUBMED   12905492
  REMARK    GeneRIF: Immature dendritic cells engulfed apoptotic and necrotic
            neutrophils, resulting in up-regulation of CD83 and class II major
            histocompatibility complex molecules, but down-regulation of CD40,
            CD80, and CD86
REFERENCE   2  (bases 1 to 2824)
  AUTHORS   Niu,H., Cattoretti,G. and Dalla-Favera,R.
  TITLE     BCL6 controls the expression of the B7-1/CD80 costimulatory
            receptor in germinal center B cells
  JOURNAL   J. Exp. Med. 198 (2), 211-221 (2003)
   PUBMED   12860928
  REMARK    GeneRIF: results show that BCL6 prevents CD40-induced expression of
            CD80 by binding its promoter region in vivo and suppressing its
            transcriptional activation by NF-kappaB
REFERENCE   3  (bases 1 to 2824)
  AUTHORS   Morichika,T., Takahashi,H.K., Iwagaki,H., Yagi,T., Saito,S.,
            Kubo,S., Yoshino,T., Akagi,T., Mori,S., Nishibori,M. and Tanaka,N.
  TITLE     Effect of prostaglandin E2 on intercellular adhesion molecule-1 and
            B7 expression in mixed lymphocyte reaction
  JOURNAL   Transplantation 75 (12), 2100-2105 (2003)
   PUBMED   12829919
  REMARK    GeneRIF: effect of PGE2 on the expression of ICAM-1 and B7 in the
            human mixed leukocyte reaction (MLR) in the presence or absence of
            IL-18
REFERENCE   4  (bases 1 to 2824)
  AUTHORS   Rogers,N.J., Jackson,I.M., Jordan,W.J., Hawadle,M.A., Dorling,A.
            and Lechler,R.I.
  TITLE     Cross-species costimulation: relative contributions of CD80, CD86,
            and CD40
  JOURNAL   Transplantation 75 (12), 2068-2076 (2003)
   PUBMED   12829914
  REMARK    GeneRIF: expression profiles and relative contribution in the
            porcine-human xenogeneic response
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REFERENCE    5   (bases 1 to 2824)
  AUTHORS    Chen,X.L., Cao,X.D., Kang,A.J., Wang,K.M., Su,B.S. and Wang,Y.L.
  TITLE      In situ expression and significance of B7 costimulatory molecules
             within tissues of human gastric carcinoma
  JOURNAL    World J. Gastroenterol. 9 (6), 1370-1373 (2003)
  PUBMED     12800259
  REMARK     GeneRIF: ICOS-B7H costimulatory pathway may be involved in the
             negative regulation of cell-mediated immune responses.
REFERENCE    6   (bases 1 to 2824)
  AUTHORS    Grosenbach,D.W., Schlom,J., Gritz,L., Gomez Yafal,A. and Hodge,J.W.
  TITLE      A recombinant vector expressing transgenes for four T-cell
             costimulatory molecules (OX40L, B7-1, ICAM-1, LFA-3) induces
             sustained CD4+ and CD8+ T-cell activation, protection from
             apoptosis, and enhanced cytokine production
  JOURNAL    Cell. Immunol. 222 (1), 45-57 (2003)
  PUBMED     12798307
  REMARK     GeneRIF: combined use of a vector driving the expression of OX40L
             with three other costimulatory molecules (B7-1, ICAM-1, and LFA-3)
             both enhances initial activation and then further potentiates
             sustained activation of nai;ve and effector T cells.
REFERENCE    7   (bases 1 to 2824)
  AUTHORS    Bernsen,M.R., Hakansson,L., Gustafsson,B., Krysander,L.,
             Rettrup,B., Ruiter,D. and Hakansson,A.
  TITLE      On the biological relevance of MHC class II and B7 expression by
             tumour cells in melanoma metastases
  JOURNAL    Br. J. Cancer 88 (3), 424-431 (2003)
  PUBMED     12569387
  REMARK     GeneRIF: On the biological relevance of MHC class II and B7
             expression by tumour cells in melanoma metastases.
REFERENCE    8   (bases 1 to 2824)
  AUTHORS    Tatari-Calderone,Z., Semnani,R.T., Nutman,T.B., Schlom,J. and
             Sabzevari,H.
  TITLE      Acquisition of CD80 by human T cells at early stages of activation:
             functional involvement of CD80 acquisition in T cell to T cell
             interaction
  JOURNAL    J. Immunol. 169 (11), 6162-6169 (2002)
  PUBMED     12444120
  REMARK     GeneRIF: data suggest that CD80 acquisition by human T cells might
             play a role in the immunoregulation of T cell responses
REFERENCE    9   (bases 1 to 2824)
  AUTHORS    Ke,X.Y., Gribben,J., Wang,J. and Wang,D.B.
  TITLE      The identical effects of B7-1 and B7-2 on regulation of human IL-2
             gene transcription factors NF-kappa B and AP-1
  JOURNAL    Zhongguo Shi Yan Xue Ye Xue Za Zhi 10 (6), 512-518 (2002)
  PUBMED     12513711
  REMARK     GeneRIF: The identical effects of B7-1 and B7-2 on regulation of
             human IL-2 gene transcription factors NF-kappa B and AP-1.
REFERENCE    10 (bases 1 to 2824)
  AUTHORS    Manzotti,C.N., Tipping,H., Perry,L.C., Mead,K.I., Blair,P.J.,
             Zheng,Y. and Sansom,D.M.
  TITLE      Inhibition of human T cell proliferation by CTLA-4 utilizes CD80
             and requires CD25+ regulatory T cells
  JOURNAL    Eur. J. Immunol. 32 (10), 2888-2896 (2002)
  PUBMED     12355442
  REMARK     GeneRIF: CD80 and CD86 differ in their interactions with CTLA-4 and
             that CD80 appears to be the preferential inhibitory ligand for
             CTLA-4 working via a population of CD4(+) CD25(+) CTLA-4(+)
             regulatory T cells.
REFERENCE    11 (bases 1 to 2824)
  AUTHORS    Akiyama,Y., Shirasugi,N., Uchida,N., Matsumoto,K., Kitajima,M.,
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                  Bashuda,H., Yagita,H., Okumura,K., Aramaki,O. and Niimi,M.
        TITLE     B7/CTLA4 pathway is essential for generating regulatory cells after
                  intratracheal delivery of alloantigen in mice
      JOURNAL     Transplantation 74 (5), 732-738 (2002)
       PUBMED     12352894
       REMARK     GeneRIF: with ctla4 pathway, is essential for generating regulatory
                  cells after intratracheal delivery of alloantigen in mice
    REFERENCE     12 (bases 1 to 2824)
      AUTHORS     Wang,S., Veldman,G.M., Stahl,M., Xing,Y., Tobin,J.F. and Erbe,D.V.
        TITLE     Antibodies to B7.1 define the GFCC'C' face of the N-terminal domain
                  as critical for co-stimulatory interactions
      JOURNAL     Immunol. Lett. 83 (2), 77-83 (2002)
       PUBMED     12067755
    REFERENCE     13 (bases 1 to 2824)
      AUTHORS     Terrazzano,G., Zanzi,D., Palomba,C., Carbone,E., Grimaldi,S.,
                  Pisanti,S., Fontana,S., Zappacosta,S. and Ruggiero,G.
        TITLE     Differential involvement of CD40, CD80, and major
                  histocompatibility complex class I molecules in cytotoxicity
                  induction and interferon-gamma production by human natural killer
                  effectors
      JOURNAL     J. Leukoc. Biol. 72 (2), 305-311 (2002)
       PUBMED     12149421
       REMARK     GeneRIF: CD40 and CD80 molecules were observed to play a specific
                  role in the induction of cytotoxic function but not in IFN-gamma
                  production of IL-2-activated NK effectors.
    REFERENCE     14 (bases 1 to 2824)
      AUTHORS     Venuprasad,K., Banerjee,P.P., Chattopadhyay,S., Sharma,S., Pal,S.,
                  Parab,P.B., Mitra,D. and Saha,B.
        TITLE     Human neutrophil-expressed CD28 interacts with macrophage B7 to
                  induce phosphatidylinositol 3-kinase-dependent IFN-gamma secretion
                  and restriction of Leishmania growth
      JOURNAL     J. Immunol. 169 (2), 920-928 (2002)
       PUBMED     12097397
       REMARK     GeneRIF: Leishmania major infection of macrophages cocultured with
                  neutrophils results in a neutrophil-macrophage interaction via CD80
                  leading to IFN-gamma secretion and restriction of Leishmania
                  growth.
    REFERENCE     15 (bases 1 to 2824)
      AUTHORS     Sellebjerg,F., Jensen,J., Jensen,C.V. and Wiik,A.
        TITLE     Expansion of CD5 - B cells in multiple sclerosis correlates with
                  CD80 (B7-1) expression
      JOURNAL     Scand. J. Immunol. 56 (1), 101-107 (2002)
       PUBMED     12100477
       REMARK     GeneRIF: expansion of CD5- B cells in multiple sclerosis correlates
                  with CD80 (B7-1) expression
    REFERENCE     16 (bases 1 to 2824)
      AUTHORS     Suvas,S., Singh,V., Sahdev,S., Vohra,H. and Agrewala,J.N.
        TITLE     Distinct role of CD80 and CD86 in the regulation of the activation
                  of B cell and B cell lymphoma
      JOURNAL     J. Biol. Chem. 277 (10), 7766-7775 (2002)
       PUBMED     11726649
       REMARK     GeneRIF: Thus, this study is the first demonstration of a distinct
                  signaling event induced by CD80 and CD86 molecules in B cell
                  lymphoma.
    REFERENCE     17 (bases 1 to 2824)
      AUTHORS     Erbe,D.V., Wang,S., Xing,Y. and Tobin,J.F.
        TITLE     Small molecule ligands define a binding site on the immune
                  regulatory protein B7.1
      JOURNAL     J. Biol. Chem. 277 (9), 7363-7368 (2002)
       PUBMED     11741888
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REMARK   GeneRIF: specific small molecule inhibitors of human B7.1 were
            identified and characterized. These compounds inhibit the binding
            of B7.1 to both CD28 and CTLA4.   .
REFERENCE   18 (bases 1 to 2824)
  AUTHORS   Vasilevko,V., Ghochikyan,A., Holterman,M.J. and Agadjanyan,M.G.
  TITLE   CD80 (B7-1) and CD86 (B7-2) are functionally equivalent in the
            initiation and maintenance of CD4+ T-cell proliferation after
            activation with suboptimal doses of PHA
  JOURNAL   DNA Cell Biol. 21 (3), 137-149 (2002)
   PUBMED   12015893
   REMARK   GeneRIF: CD80 and CD86 molecules can substitute for each other in
            the initial activation of resting CD4(+) T cells and in the
            maintenance of their proliferative response
REFERENCE   19 (bases 1 to 2824)
  AUTHORS   Pesce,G., Fiorino,N., Riccio,A.M., Montagna,P., Torre,G.,
            Salmaso,C., Altrinetti,V. and Bagnasco,M.
  TITLE   Different intrathyroid expression of intercellular adhesion
            molecule-1 (ICAM-1) in Hashimoto's thyroiditis and Graves' disease:
            analysis at mRNA level and association with B7.1 costimulatory
            molecule
  JOURNAL   J. Endocrinol. Invest. 25 (3), 289-295 (2002)
   PUBMED   11936473
   REMARK   GeneRIF: colocalization of ICAM-1 and B7.1 molecules was   .
            demonstrated in Hashomoto's thyroiditis whereas no B7.1 expression
            was observed in Graves' disease
REFERENCE   20 (bases 1 to 2824)
  AUTHORS   Tzachanis,D., Berezovskaya,A., Nadler,L.M. and Boussiotis,V.A.
  TITLE   Blockade of B7/CD28 in mixed lymphocyte reaction cultures results
            in the generation of alternatively activated macrophages, which
            suppress T-cell responses
  JOURNAL   Blood 99 (4), 1465-1473 (2002)
   PUBMED   11830501
   REMARK   GeneRIF: Blockade of B7/CD28 costimulation in mixed lymphocyte
            reaction cultures results in the generation of alternatively
            activated macrophages, which suppress T-cell responses,and perhaps
            play a critical role in the induction of transplantation tolerance.
REFERENCE   21 (bases 1 to 2824)
  AUTHORS   Niemann-Masanek,U., Mueller,A., Yard,B.A., Waldherr,R. and van der
            Woude,F.J.
  TITLE   B7-1 (CD80) and B7-2 (CD 86) expression in human tubular epithelial
            cells in vivo and in vitro
  JOURNAL   Nephron 92 (3), 542-556 (2002)
   PUBMED   12372936
   REMARK   GeneRIF: After B7-1 and B7-2 induction, proximal tubular epithelial
            cells costimulate CD28 on T lymphocytes resulting in cytokine
            production.
REFERENCE   22 (bases 1 to 2824)
  AUTHORS   Chang,T.T., Kuchroo,V.K. and Sharpe,A.H.
  TITLE   Role of the B7-CD28/CTLA-4 pathway in autoimmune disease
  JOURNAL   Curr. Dir. Autoimmun. 5, 113-130 (2002)
   PUBMED   11826754   .
   REMARK   GeneRIF: The B7-CD28/CTLA-4 costimulatory pathway has a dominant
            role in regulating T-cell activation. Antagonists enable graft
            survival and suppress autoimmunity.
REFERENCE   23 (bases 1 to 2824)
  AUTHORS   Reeves,R.H., Patch,D., Sharpe,A.H., Borriello,F., Freeman,G.J.,
            Edelhoff,S. and Disteche,C.
  TITLE   The costimulatory genes Cd80 and Cd86 are linked on mouse
            chromosome 16 and human chromosome 3
  JOURNAL   Mamm. Genome 8 (8), 581-582 (1997)

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    PUBMED     9250865
 REFERENCE     24 (bases 1 to 2824)
   AUTHORS     Freeman,G.J., Disteche,C.M., Gribben,J.G., Adler,D.A.,
               Freedman,A.S., Dougery,J. and Nadler,L.M.
     TITLE     The gene for B7, a costimulatory signal for T-cell activation, maps
               to chromosomal region 3q13.3-3q21
   JOURNAL     Blood 79 (2), 489-494 (1992)
    PUBMED     1370389
 REFERENCE     25 (bases 1 to 2824)
   AUTHORS     Selvakumar,A., Mohanraj,B.K., Eddy,R.L., Shows,T.B., White,P.C. and
               Dupont,B.
     TITLE     Genomic organization and chromosomal location of the human gene
               encoding the B-lymphocyte activation antigen B7
   JOURNAL     Immunogenetics 36 (3), 175-181 (1992)
    PUBMED     1377173
 REFERENCE     26 (bases 1 to 2824)
   AUTHORS     Freeman,G.J., Freedman,A.S., Segil,J.M., Lee,G., Whitman,J.F. and
               Nadler,L.M.
     TITLE     B7, a new member of the Ig superfamily with unique expression on
               activated and neoplastic B cells
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Jun 8 2004 17:01:12

NCBI   **results of BLAST**

BLASTN 2.2.9 [May-01-2004]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
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"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1089397280-30589-192748561519.BLASTQ4

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If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 165 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores

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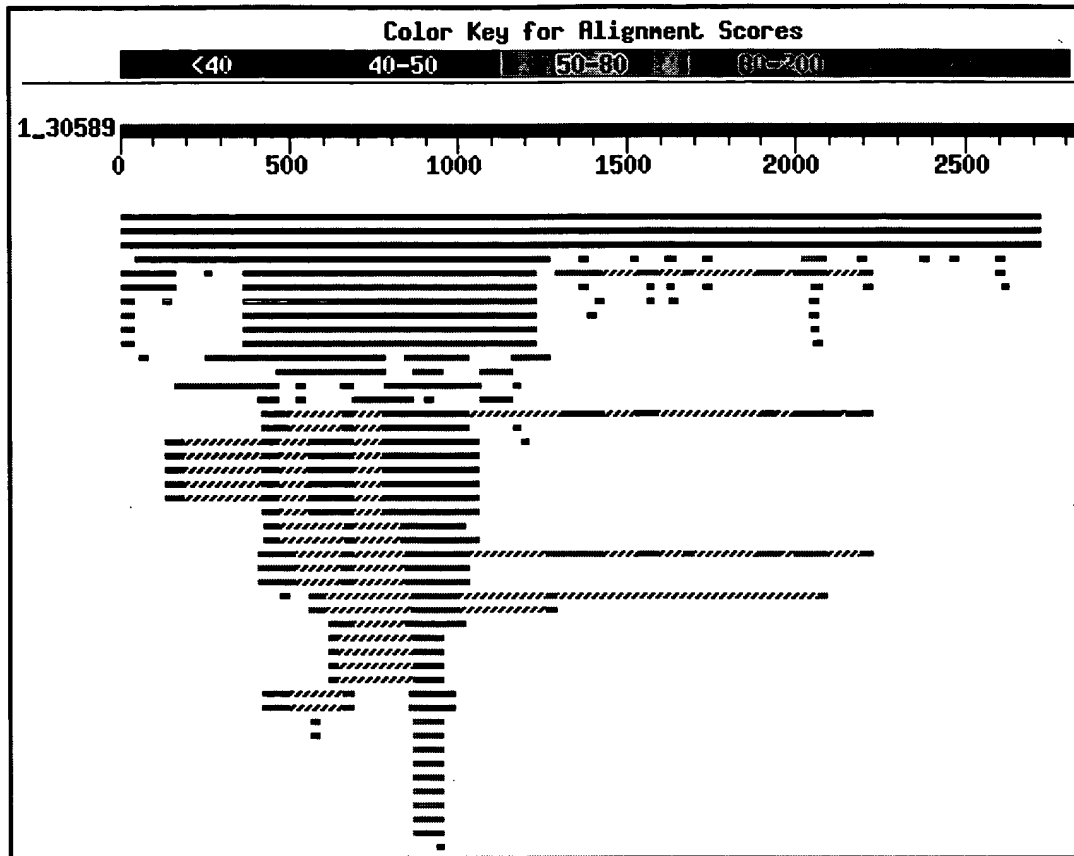
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gi|22651512|gb|AY081815.1| Homo sapiens costimulatory molec...	1027	0.0	U
gi|179324|gb|M83073.1|HUMB7AN03 Homo sapiens antigen B7 gen...	634	e-178	
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gi|179325|gb|M83074.1|HUMB7AN04 Homo sapiens antigen B7 gen...	563	e-157	
gi|1262191|gb|U33208.1|HSU33208 Human B-lymphocyte activati...	325	3e-85	G
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gi|46849851|gb|AY591920.1| Macaca fascicularis CD80 mRNA, p...	317	7e-83	
gi|2065520|gb|U57755.1|FCU57755 Felis catus T-cell specific...	254	9e-64	
gi|9796385|dbj|AB030651.1| Felis catus mRNA for B-lymphocyt...	254	9e-64	
gi|6653506|gb|AF203443.1|AF203443 Sus scrofa CD80 protein p...	226	2e-55	L U
gi|6653504|gb|AF203442.1|AF203442 Sus scrofa CD80 protein p...	226	2e-55	U
gi|18072036|gb|AF455811.1| Sus scrofa CD80 (CD80) mRNA, com...	226	2e-55	L U

gi|8100070|dbj|AB038153.2| Sus scrofa mRNA for CD80 protein...   226   2e-55 [U]
gi|13591561|dbj|AB049760.1| Sus scrofa CD80/B7-1 mRNA for C...   226   2e-55 [L][U]
gi|8100061|dbj|AB026121.2| Sus scrofa mRNA for CD80 protein...   226   2e-55 [U]
gi|179327|gb|M83077.1|HUMB7AN06   Homo sapiens antigen B7 gen...   220   1e-53 [L]
gi|22775283|gb|AF536987.1| Synthetic construct CD28 binding...   216   2e-52
gi|2677623|emb|Y09950.1|BTCD80   B.taurus CD80 mRNA   202   3e-48 [L][U]
gi|1685044|gb|U72535.1|HSU72535   Homo sapiens LIM domain pro...   192   3e-45 [L]
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gi|7739770|gb|AF257653.1|AF257653   Canis familiaris T-cell c...   163   3e-36 [U]
gi|6572505|gb|AF106831.1|CFCD80Y4   Canis familiaris secreted...   163   3e-36
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gi|25188155|dbj|AB085743.1| Mesocricetus auratus B7-1b mRNA...   123   2e-24
gi|25188153|dbj|AB085742.1| Mesocricetus auratus B7-1a mRNA...   123   2e-24
gi|6572508|gb|AF106834.1|CFCD80Y7   Canis familiaris B7-1 pro...   107   1e-19 [G]
gi|755096|dbj|D49843.1|RABCD80C   Oryctolagus cuniculus mRNA ...   101   8e-18
gi|507872|gb|U10925.1|RNU10925   Rattus norvegicus NEDH B7-1 ...   95   5e-16 [L][U][G]
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gi|29789033|ref|NM_012926.1| Rattus norvegicus CD80 antigen...   87   1e-13 [L][U]
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gi|30268719|gb|AF387763.1| Meriones unguiculatus costimulat...   83   2e-12
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gi|10566942|dbj|AB033127.1| Homo sapiens CD80 gene, promote...   81   7e-12
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gi|47084437|gb|AC107274.11| Rattus norvegicus 18 BAC CH230-...   75   5e-10
gi|31982960|ref|NM_009855.1| Mus musculus CD80 antigen (Cd8...   57   1e-04 [L][U]
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gi|50111|emb|X60958.1|MMB7BLAA   Mouse B7 mRNA for B lymphocy...   57   1e-04 [L][U][G]
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gi|15418723|gb|AY007703.1| Felis catus CD80 (CD80) mRNA, co...   54   0.002
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gi|7768735|dbj|AP001743.1| Homo sapiens genomic DNA, chromo...   48   0.10 [G]
gi|7670569|dbj|AP001615.1| Homo sapiens genomic DNA, chromo...   48   0.10 [L]
gi|33342319|gb|AC138134.6| Mus musculus clone rp23-382i2 ma...   46   0.41
gi|46931443|gb|AC102091.7| Mus musculus chromosome 18, clon...   46   0.41
gi|32398575|emb|BX293563.9| Mouse DNA sequence from clone R...   46   0.41
gi|6572504|gb|AF106830.1|CFCD80Y3   Canis familiaris B7-1 pro...   46   0.41
gi|29124247|gb|AC127228.3| Mus musculus BAC clone RP24-539P...   44   1.6
gi|37777384|gb|AC110541.12| Mus musculus chromosome 7, clon...   44   1.6
gi|34367929|emb|BX648765.1|HSM808916   Homo sapiens mRNA; cDN...   44   1.6 [U]
gi|10443448|emb|AL359412.12| Human DNA sequence from clone ...   44   1.6

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gi|20068706|emb|AL669876.7|    Human DNA sequence from clone R...     42    6.4
gi|20068679|emb|AL663033.10|   Mouse DNA sequence from clone ...      42    6.4
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Alignments

[Get selected sequences]   [Select all]   [Deselect all]

☐ >gi|27503575|gb|BC042665.1| L U Homo sapiens CD80 antigen (CD28 antigen ligand 1
        (cDNA clone MGC:34467 IMAGE:5181343), complete cds
        Length = 2824

Score = 5356 bits (2702), Expect = 0.0
Identities = 2716/2723 (99%)
Strand = Plus / Plus

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Query: 2401 ctcatggcagctaagccacatggctgggatttaaagcctttagagccagcccatggcttt 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2401 ctcatggcagctaagccacatggctgggatttaaagcctttagagccagcccatggcttt 2460


Query: 2461 agctacctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgt 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2461 agctacctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgt 2520


Query: 2521 agggcagagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaa 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2521 agggcagagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaa 2580


Query: 2581 tacttaactcaataattcttttcttttccatttagtaacagttgtgatgactatgtttct 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2581 tacttaactcaataattcttttcttttccatttagtaacagttgtgatgactatgtttct 2640


Query: 2641 attctaagtaattcctgtattctacagcagatactttgtcagcaatactaagggaagaaa 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2641 attctaagtaattcctgtattctacagcagatactttgtcagcaatactaagggaagaaa 2700


Query: 2701 caaagttgaaccgtttctttaat 2723
             |||||||||||||||||||||||
Sbjct: 2701 caaagttgaaccgtttctttaat 2723
```


☐ >gi|31377790|ref|NM_005191.2| 🅻 🅄🄶 Homo sapiens CD80 antigen (CD28 antigen liga
             (CD80), mRNA
          Length = 2824

 Score = 5356 bits (2702), Expect = 0.0
 Identities = 2716/2723 (99%)
 Strand = Plus / Plus


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Query: 1    aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 60


Query: 61   atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120


Query: 121  aaatcaaaggatttaaagaaaaagtggaattttcttcagcaagctgtgaaactaaatcc 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  aaatcaaaggatttaaagaaaaagtggaattttcttcagcaagctgtgaaactaaatcc 180
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Query: 181  acaacctttggagacccaggaacaccctccaatctctgtgtgtttttgtaaacatcactgg 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  acaacctttggagacccaggaacaccctccaatctctgtgtgtttttgtaaacatcactgg 240


Query: 241  agggtcttctacgtgagcaattggattgtcatcagccctgcctgttttgcacctgggaag 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  agggtcttctacgtgagcaattggattgtcatcagccctgcctgttttgcacctgggaag 300


Query: 301  tgccctggtcttacttgggtccaaattgttggctttcacttttgaccctaagcatctgaa 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  tgccctggtcttacttgggtccaaattgttggctttcacttttgaccctaagcatctgaa 360


Query: 361  gccatgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttc 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  gccatgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttc 420


Query: 421  tttcagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgacc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  tttcagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgacc 480


Query: 481  aaggaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctg 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  aaggaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctg 540


Query: 541  gcacaaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggg 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  gcacaaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggg 600


Query: 601  gacatgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctc 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  gacatgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctc 660


Query: 661  tccattgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctg 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  tccattgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctg 720


Query: 721  aagtatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaa 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  aagtatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaa 780


Query: 781  gctgacttccctacacctagtatatctgactttgaaattccaacttctaatattagaagg 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  gctgacttccctacacctagtatatctgactttgaaattccaacttctaatattagaagg 840


Query: 841  ataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatgga 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  ataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatgga 900
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Query:  901  gaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgct  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  901  gaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgct  960


Query:  961  gttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaag  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  961  gttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaag  1020


Query: 1021  tatggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcatttt  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021  tatggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcatttt  1080


Query: 1081  cctgataacctgctcccatcctgggccattaccttaatctcagtaaatggaatttttgtg  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081  cctgataacctgctcccatcctgggccattaccttaatctcagtaaatggaatttttgtg  1140


Query: 1141  atatgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagaga  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141  atatgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagaga  1200


Query: 1201  ttgagaagggaaagtgtacgccctgtataacagtgtccgcagaagcaaggggctgaaaag  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201  ttgagaagggaaagtgtacgccctgtataacagtgtccgcagaagcaaggggctgaaaag  1260


Query: 1261  atctgaaggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggaca  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261  atctgaaggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggaca  1320


Query: 1321  agattaccccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgct  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321  agattaccccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgct  1380


Query: 1381  ttgcaggaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatca  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381  ttgcaggaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatca  1440


Query: 1441  aggggttttgaaatgcagaattcttgagttctggaagggactttagagaataccagtgtt  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441  aggggttttgaaatgcagaattcttgagttctggaagggactttagagaataccagtgtt  1500


Query: 1501  attaatgacaaaggcactgaggcccagggaggtgacccgaattataaaggccagcgccag  1560
             |||||||||||||||||||||||||||||||||||||||||||||||.||||||||||||
Sbjct: 1501  attaatgacaaaggcactgaggcccagggaggtgacccgaattataaaggccagcgccag  1560


Query: 1561  aacccagatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaa  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1561  aacccagatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaa  1620
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Query: 1621  ctggtatatacatatatatgtcaggcaaagtgctgctggaagtagaatttgtccaataac 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1621  ctggtatatacatatatatgtcaggcaaagtgctgctggaagtagaatttgtccaataac 1680


Query: 1681  aggtcaacttcagagactatctgatttcctaatgtcagagtagaagattttatgctgctg 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1681  aggtcaacttcagagactatctgatttcctaatgtcagagtagaagattttatgctgctg 1740


Query: 1741  tttacaaaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaat 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1741  tttacaaaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaat 1800


Query: 1801  ggaaatattattggtgtttacccagtattccannnnnnnncattgtgttctctattgctgc 1860
              ||||||||||||||||||||||||||||||||||         |||||||||||||||||||
Sbjct: 1801  ggaaatattattggtgtttacccagtattccattttttttcattgtgttctctattgctgc 1860


Query: 1861  tctctcactcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctg 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1861  tctctcactcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctg 1920


Query: 1921  acatgtaagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtc 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1921  acatgtaagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtc 1980


Query: 1981  caaagacttaactggttcatattggactgataatctctttaaatggctttatgctagttt 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1981  caaagacttaactggttcatattggactgataatctctttaaatggctttatgctagttt 2040


Query: 2041  gacctcatttgtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttaca 2100
              |||||||||||||||||||||||||||||||||||||||||||||||||||.|||||||||
Sbjct: 2041  gacctcatttgtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttaca 2100


Query: 2101  gtgtatgtactaagcagtaagctatcttcaaatgtctaaggtagtaactttccatagggc 2160
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Sbjct: 2101  gtgtatgtactaagcagtaagctatcttcaaatgtctaaggtagtaactttccatagggc 2160


Query: 2161  ctccttagatccctaagatggcttttctccttggtatttctgggtctttctgacatcag 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2161  ctccttagatccctaagatggcttttctccttggtatttctgggtctttctgacatcag 2220


Query: 2221  cagagaactggaaagacatagccaactgctgttcatgttactcatgactcctttctctaa 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2221  cagagaactggaaagacatagccaactgctgttcatgttactcatgactcctttctctaa 2280


Query: 2281  aactgccttccacaattcactagaccagaagtggacgcaacttaagctgggataatcaca 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2281  aactgccttccacaattcactagaccagaagtggacgcaacttaagctgggataatcaca 2340
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Query: 2341  ttatcatctgaaaatctggagttgaacagcaaaagaagacaacatttctcaaatgcacat 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2341  ttatcatctgaaaatctggagttgaacagcaaaagaagacaacatttctcaaatgcacat 2400


Query: 2401  ctcatggcagctaagccacatggctgggatttaaagcctttagagccagcccatggcttt 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2401  ctcatggcagctaagccacatggctgggatttaaagcctttagagccagcccatggcttt 2460


Query: 2461  agctacctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgt 2520
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Sbjct: 2461  agctacctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgt 2520


Query: 2521  agggcagagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaa 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2521  agggcagagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaa 2580


Query: 2581  tacttaactcaataattcttttcttttccatttagtaacagttgtgatgactatgtttct 2640
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Sbjct: 2581  tacttaactcaataattcttttcttttccatttagtaacagttgtgatgactatgtttct 2640


Query: 2641  attctaagtaattcctgtattctacagcagatactttgtcagcaatactaagggaagaaa 2700
             |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2641  attctaagtaattcctgtattctacagcagatactttgtcagcaatactaagggaagaaa 2700


Query: 2701  caaagttgaaccgtttctttaat 2723
             |||||||||||||||||||||||
Sbjct: 2701  caaagttgaaccgtttctttaat 2723
```

☐ >gi|19033385|gb|AC073352.22| 🔲 Homo sapiens 3 BAC RP11-190C22 (Roswell Park Canc
              Library) complete sequence
        Length = 159738

 Score = 2831 bits (1428), Expect = 0.0
 Identities = 1448/1457 (99%)
 Strand = Plus / Plus

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Query: 1267    aggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggacaagatta 1326
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 116804  aggtcccacctccatttgcaattgacctcttctgggaacttcctcagatggacaagatta 116863


Query: 1327    ccccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgctttgcag 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 116864  ccccaccttgccctttacgtatctgctcttaggtgcttcttcacttcagttgctttgcag 116923


Query: 1387    gaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatcaaggggt 1446
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 116924  gaagtgtctagaggaatatggtgggcacagaagtagctctggtgaccttgatcaaggtgt 116983
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Query:  1447   tttgaaatgcagaattcttgagttctggaagggactttagagaataccagtgttattaat  1506
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  116984 tttgaaatgcagaattcttgagttctggaagggactttagagaataccagtgttattaat  117043


Query:  1507   gacaaaggcactgaggcccagggaggtgacccgaattataaaggccagcgccagaaccca  1566
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117044 gacaaaggcactgaggcccagggaggtgacccgaattataaaggccagcgccagaaccca  117103


Query:  1567   gatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaactggta  1626
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117104 gatttcctaactctggtgctctttccctttatcagtttgactgtggcctgttaactggta  117163


Query:  1627   tatacatatatatgtcaggcaaagtgctgctggaagtagaatttgtccaataacaggtca  1686
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117164 tatacatatatatgtcaggcaaagtgctgctggaagtagaatttgtccaataacaggtca  117223


Query:  1687   acttcagagactatctgatttcctaatgtcagagtagaagattttatgctgctgtttaca  1746
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117224 acttcagagactatctgatttcctaatgtcagagtagaagattttatgctgctgtttaca  117283


Query:  1747   aaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaatggaaat  1806
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117284 aaagcccaatgtaatgcataggaagtatggcatgaacatctttaggagactaatggaaat  117343


Query:  1807   attattggtgtttacccagtattccannnnnnnncattgtgttctctattgctgctctctc  1866
               ||||||||||||||||||||||||||      |||||||||||||||||||||||||||||
Sbjct:  117344 attattggtgtttacccagtattccatttttttcattgtgttctctattgctgctctctc  117403


Query:  1867   actcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctgacatgt  1926
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117404 actcccccatgaggtacagcagaaaggagaactatccaaaactaatttcctctgacatgt  117463


Query:  1927   aagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtccaaaga  1986
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117464 aagacgaatgatttaggtacgtcaaagcagtagtcaaggaggaaagggatagtccaaaga  117523


Query:  1987   cttaactggttcatattggactgataatctctttaaatggctttatgctagtttgacctc  2046
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117524 cttaactggttcatattggactgataatctctttaaatggctttatgctagtttgacctc  117583


Query:  2047   atttgtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttacagtgtat  2106
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117584 atttgtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttacagtgtat  117643


Query:  2107   gtactaagcagtaagctatcttcaaatgtctaaggtagtaactttccatagggcctcctt  2166
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  117644 gtactaagcagtaagctatcttcaaatgtctaaggtagtaactttccatagggcctcctt  117703
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Query: 2167   agatccctaagatggcttttctccttggtatttctgggtctttctgacatcagcagaga 2226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 117704 agatccctaagatggcttttctccttggtatttctgggtctttctgacatcagcagaga 117763


Query: 2227   actggaaagacatagccaactgctgttcatgttactcatgactcctttctctaaaactgc 2286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 117764 actggaaagacatagccaactgctgttcatgttactcatgactcctttctctaaaactgc 117823


Query: 2287   cttccacaattcactagaccagaagtggacgcaacttaagctgggataatcacattatca 2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 117824 cttccacaattcactagaccagaagtggacgcaacttaagctgggataatcacattatca 117883


Query: 2347   tctgaaaatctggagttgaacagcaaaagaagacaacatttctcaaatgcacatctcatg 2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 117884 tctgaaaatctggagttgaacagcaaaagaagacaacatttctcaaatgcacatctcatg 117943


Query: 2407   gcagctaagccacatggctgggatttaaagcctttagagccagcccatggctttagctac 2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 117944 gcagctaagccacatggctgggatttaaagcctttagagccagcccatggctttagctac 118003


Query: 2467   ctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgtagggca 2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 118004 ctcactatgctgcttcacaaaccttgctcctgtgtaaaactatattctcagtgtagggca 118063


Query: 2527   gagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaatactta 2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 118064 gagaggtctaacaccaacataaggtactagcagtgtttcccgtattgacaggaatactta 118123


Query: 2587   actcaataattcttttcttttccatttagtaacagttgtgatgactatgtttctattcta 2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 118124 actcaataattcttttcttttccatttagtaacagttgtgatgactatgtttctattcta 118183


Query: 2647   agtaattcctgtattctacagcagatactttgtcagcaatactaagggaagaaacaaagt 2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 118184 agtaattcctgtattctacagcagatactttgtcagcaatactaagggaagaaacaaagt 118243


Query: 2707   tgaaccgtttctttaat 2723
              |||||||||||||||||
Sbjct: 118244 tgaaccgtttctttaat 118260
```

```
Score =  634 bits (320), Expect = e-178
Identities = 320/320 (100%)
Strand = Plus / Plus
```

```
Query: 462    aggtgttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaa 521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct:  97686  aggtgttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaa  97745


Query:    522  tgtttctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggt  581
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  97746  tgtttctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggt  97805


Query:    582  gctgactatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctt  641
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  97806  gctgactatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctt  97865


Query:    642  tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac  701
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  97866  tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac  97925


Query:    702  atacgagtgtgttgttctgaagtatgaaaaagacgctttcaagcgggaacacctggctga  761
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  97926  atacgagtgtgttgttctgaagtatgaaaaagacgctttcaagcgggaacacctggctga  97985


Query:    762  agtgacgttatcagtcaaag  781
               ||||||||||||||||||||
Sbjct:  97986  agtgacgttatcagtcaaag  98005
```

```
 Score =  599 bits (302), Expect = e-167
 Identities = 302/302 (100%)
 Strand = Plus / Plus
```

```
Query:    164  gctgtgaaactaaatccacaacctttggagacccaggaacaccctccaatctctgtgtgt  223
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  84627  gctgtgaaactaaatccacaacctttggagacccaggaacaccctccaatctctgtgtgt  84686


Query:    224  tttgtaaacatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcct  283
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  84687  tttgtaaacatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcct  84746


Query:    284  gttttgcacctgggaagtgccctggtcttacttgggtccaaattgttggctttcactttt  343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  84747  gttttgcacctgggaagtgccctggtcttacttgggtccaaattgttggctttcactttt  84806


Query:    344  gaccctaagcatctgaagccatgggccacacacggaggcagggaacatcaccatccaagt  403
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  84807  gaccctaagcatctgaagccatgggccacacacggaggcagggaacatcaccatccaagt  84866


Query:    404  gtccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcag  463
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  84867  gtccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcag  84926


Query:    464  gt  465
```

```
             ||
Sbjct: 84927 gt 84928
```

```
Score =  563 bits (284), Expect = e-157
Identities = 284/284 (100%)
Strand = Plus / Plus
```

```
Query: 780    agctgacttccctacacctagtatatctgactttgaaattccaacttctaatattagaag 839
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 105135 agctgacttccctacacctagtatatctgactttgaaattccaacttctaatattagaag 105194
```

```
Query: 840    gataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatgg 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 105195 gataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatgg 105254
```

```
Query: 900    agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 105255 agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 105314
```

```
Query: 960    tgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 1019
              ||||||||||||.|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 105315 tgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 105374
```

```
Query: 1020   gtatggacatttaagagtgaatcagaccttcaactggaatacaa 1063
              |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 105375 gtatggacatttaagagtgaatcagaccttcaactggaatacaa 105418
```

```
Score =  325 bits (164), Expect = 3e-85
Identities = 164/164 (100%)
Strand = Plus / Plus
```

```
Query: 1      aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 82953  aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 83012
```

```
Query: 61     atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83013  atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 83072
```

```
Query: 121    aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 164
              ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 83073  aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 83116
```

```
Score =  220 bits (111), Expect = 1e-53
Identities = 111/111 (100%)
Strand = Plus / Plus
```

```
Query: 1160   gctttgccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114714 gctttgccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 114773


Query: 1220   gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 1270
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114774 gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 114824
```

```
 Score =  192 bits (97), Expect = 3e-45
 Identities = 97/97 (100%)
 Strand = Plus / Plus
```

```
Query: 1064   ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag 1123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 112618 ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag 112677


Query: 1124   taaatggaattttttgtgatatgctgcctgacctactg 1160
              ||||||||||||||||||||||||||||||||||||||
Sbjct: 112678 taaatggaattttttgtgatatgctgcctgacctactg 112714
```

☐ >gi|184680|gb|M27533.1|HUMIGB7 🅛🅤🅖 Human Ig rearranged B7 protein mRNA VC1-reg
            Length = 1491

```
 Score = 2426 bits (1224), Expect = 0.0
 Identities = 1224/1224 (100%)
 Strand = Plus / Plus
```

```
Query: 47    ccaaagaaaaagtgatttgtcattgctttatagactgtaagaagagaacatctcagaagt 106
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1     ccaaagaaaaagtgatttgtcattgctttatagactgtaagaagagaacatctcagaagt 60


Query: 107   ggagtcttaccctgaaatcaaaggatttaaagaaaaagtggaattttttcttcagcaagct 166
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61    ggagtcttaccctgaaatcaaaggatttaaagaaaaagtggaattttttcttcagcaagct 120


Query: 167   gtgaaactaaatccacaacctttggagacccaggaacaccctccaatctctgtgtgtttt 226
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   gtgaaactaaatccacaacctttggagacccaggaacaccctccaatctctgtgtgtttt 180


Query: 227   gtaaacatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcctgtt 286
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   gtaaacatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcctgtt 240


Query: 287   ttgcacctgggaagtgccctggtcttacttgggtccaaattgttggctttcacttttgac 346
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   ttgcacctgggaagtgccctggtcttacttgggtccaaattgttggctttcacttttgac 300
```

```
Query: 347   cctaagcatctgaagccatgggccacacacggaggcagggaacatcaccatccaagtgtc 406
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   cctaagcatctgaagccatgggccacacacggaggcagggaacatcaccatccaagtgtc 360


Query: 407   catacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggtg 466
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361   catacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggtg 420


Query: 467   ttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaatgttt 526
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421   ttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaatgttt 480


Query: 527   ctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggtgctga 586
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481   ctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggtgctga 540


Query: 587   ctatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctttgata 646
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541   ctatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctttgata 600


Query: 647   tcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcacatacg 706
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601   tcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcacatacg 660


Query: 707   agtgtgttgttctgaagtatgaaaaagacgctttcaagcgggaacacctggctgaagtga 766
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661   agtgtgttgttctgaagtatgaaaaagacgctttcaagcgggaacacctggctgaagtga 720


Query: 767   cgttatcagtcaaagctgacttccctacacctagtatatctgactttgaaattccaactt 826
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721   cgttatcagtcaaagctgacttccctacacctagtatatctgactttgaaattccaactt 780


Query: 827   ctaatattagaaggataaatttgctcaacctctggaggttttccagagcctcacctctcct 886
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781   ctaatattagaaggataaatttgctcaacctctggaggttttccagagcctcacctctcct 840


Query: 887   ggttggaaaatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaa 946
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841   ggttggaaaatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaa 900


Query: 947   ctgagctctatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttca 1006
             |||||||||||||||||||||||||||||||||||||||·||||||||||||||||||||
Sbjct: 901   ctgagctctatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttca 960


Query: 1007  tgtgtctcatcaagtatggacatttaagagtgaatcagaccttcaactggaatacaacca 1066
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961   tgtgtctcatcaagtatggacatttaagagtgaatcagaccttcaactggaatacaacca 1020
```

```
Query: 1067  agcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcagtaa 1126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021  agcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcagtaa 1080


Query: 1127  atggaatttttgtgatatgctgcctgacctactgctttgccccaagatgcagagagagaa 1186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081  atggaatttttgtgatatgctgcctgacctactgctttgccccaagatgcagagagagaa 1140


Query: 1187  ggaggaatgagagattgagaagggaaagtgtacgccctgtataacagtgtccgcagaagc 1246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141  ggaggaatgagagattgagaagggaaagtgtacgccctgtataacagtgtccgcagaagc 1200


Query: 1247  aaggggctgaaaagatctgaaggt 1270
              ||||||||||||||||||||||||
Sbjct: 1201  aaggggctgaaaagatctgaaggt 1224
```

☐ >gi|22775285|gb|AF536988.1| Synthetic construct CTLA-4 binding protein precursor
            complete cds
          Length = 867

 Score = 1556 bits (785), Expect = 0.0
 Identities = 845/865 (97%)
 Strand = Plus / Plus

```
Query: 364  atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttcttt 423
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct: 1    atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaagttcttt 60


Query: 424  cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag 483
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag 120


Query: 484  gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 180


Query: 544  caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 603
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  caaactcgcatccactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 240


Query: 604  atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 300


Query: 664  attgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 723
             || |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  atcgtgattctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 360
```

```
Query: 724   tatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaagct 783
             ||||||||||| ||||||||| |||||||||||||||||||||| ||||||| ||||||||||
Sbjct: 361   tatgaaaaagatgctttcaagcgagaacacctggctgaagtgatgttatccgtcaaagct 420


Query: 784   gacttccctacacctagtatatctgactttgaaattccaacttctaatattagaaggata 843
             |||||||||||||||||||||||||||||||||||||||||| ||||||| |||||||||||
Sbjct: 421   gacttccctacacctagtatatctgactttgaaattccaccttctaacattagaaggata 480


Query: 844   atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa 903
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||| |||
Sbjct: 481   atttgctcaacctctggaggttttccagagcctcacctcttctggttggaaaatggggaa 540


Query: 904   gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgtt 963
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 541   gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatactgtt 600


Query: 964   agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat 1023
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601   agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat 660


Query: 1024  ggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcattttcct 1083
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct: 661   ggacatttaagagtgaatcagaccttcaactggaatacacccaagcaagagcattttcct 720


Query: 1084  gataacctgctcccatcctgggccattaccttaatctcagtaaatggaattttttgtgata 1143
             ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 721   gataacctgctcccatcctgggccattaccttaatctcagcaaatggaatttttgtgata 780


Query: 1144  tgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagagattg 1203
             ||||||||||||| |||||||||||||||||||||||||||||| ||| ||||||| | ||
Sbjct: 781   tgctgcctgacctaccgctttgccccaagatgcagagagagaaagagcaatgagacactg 840


Query: 1204  agaagggaaagtgtacgccctgtat 1228
             |||||||||||||||||||||||||
Sbjct: 841   agaagggaaagtgtacgccctgtat 865
```

☐ >gi|3414976|gb|AF079519.1|AF079519　　Macaca nemestrina B7 protein (B7) mRNA, compl
　　　　　Length = 867

Score = 1548 bits (781), Expect = 0.0
Identities = 844/865 (97%)
Strand = Plus / Plus

```
Query: 364   atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttcttt 423
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||
Sbjct: 1     atgggccacacacggaggcagggaatctcaccatccaagtgtccatacctcaagttcttt 60
```

```
Query: 424   cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag 483
             |||||||||||||||||||| ||||||||||| |||||||||||||||||||||||||||||
Sbjct: 61    cagctcttggtgctggcttgtctttctcatttctgttcaggtgttatccacgtgaccaag 120


Query: 484   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 180


Query: 544   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 240


Query: 604   atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 663
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct: 241   atgaatatatggcccgagtacaagaaccggaccatctttgatatcacgaataacctctcc 300


Query: 664   attgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 723
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   attgtgattctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 360


Query: 724   tatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaagct 783
             |||||||||| |||||||||||||||||||||||||||||||||| |||||| |||||||
Sbjct: 361   tatgaaaaagatgctttcaagcgggaacacctggctgaagtgatgttatccgtcaaagct 420


Query: 784   gacttccctacacctagtatatctgactttgaaattccaacttctaatattagaaggata 843
             ||||||||||||||||||||| ||||||||||||||||||| ||||||| ||||||||||
Sbjct: 421   gacttccctacacctagtataactgactttgaaattccaccttctaacattagaaggata 480


Query: 844   atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa 903
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481   atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa 540


Query: 904   gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgtt 963
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 541   gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatactgtt 600


Query: 964   agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat 1023
             ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Sbjct: 601   agcagcaaactggatttcaatatgacaaccaatcacagtttcatgtgtctcatcaagtat 660


Query: 1024  ggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcattttcct 1083
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct: 661   ggacatttaagagtgaatcagaccttcaactggaatacacccaagcaagagcattttcct 720


Query: 1084  gataacctgctcccatcctgggccattaccttaatctcagtaaatggaatttttgtgata 1143
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct: 721   gataacctgctcccatcctgggccattaccctaatctcagtaaatggaattttttgtgata 780
```

```
Query: 1144  tgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagagattg 1203
              ||||||||||||||||| |||||||||||||||||||||||||||| ||||||||| ||||
Sbjct: 781   tgctgcctgacctactgttttgccccaagatgcagagagagaagaaggaatgagacattg 840


Query: 1204  agaagggaaagtgtacgccctgtat 1228
              |||||||||||||||||||||||||
Sbjct: 841   agaagggaaagtgtacgccctgtat 865
```

☐ >gi|13655486|gb|AF344849.1|AF344849   Macaca mulatta CD80 protein precursor (N939)
            Length = 867

 Score = 1501 bits (757), Expect = 0.0
 Identities = 838/865 (96%)
 Strand = Plus / Plus

```
Query: 364   atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttcttt 423
             ||||||||||||||||||||||||| || ||||||||||||||||||||||||| ||||||
Sbjct: 1     atgggccacacacggaggcaggaaatatcaccatccaagtgtccatacctcaagttcttt 60


Query: 424   cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag 483
             |||||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||
Sbjct: 61    cagctcttggtgctggcttgtctttctcatttctgttcaggtgttatccacgtgaccaag 120


Query: 484   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 180


Query: 544   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 240


Query: 604   atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 663
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct: 241   atgaatatatggcccgagtacaagaaccggaccatctttgatatcacaaataacctctcc 300


Query: 664   attgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 723
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   attgtgattctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 360


Query: 724   tatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaagct 783
             |||||||||| ||||||||||||||||||||||||||||||||||| |||||| |||||||
Sbjct: 361   tatgaaaaagatgctttcaagcgggaacacctggctgaagtgatgttatccgtcaaagct 420


Query: 784   gacttccctacacctagtatatctgactttgaaattccaacttctaatattagaaggata 843
             ||||||||||||||||||||| |||||| |||||||||| ||||||| ||||||||||||
Sbjct: 421   gacttccctacacctagtataactgactctgaaattccaccttctaacattagaaggata 480
```

```
Query: 844  atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa  903
            ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  atttgctcaaactctggaggttttccagagcctcacctctcctggttggaaaatggagaa  540


Query: 904  gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgtt  963
            ||||||||||||||| ||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 541  gaattaaatgccatcagcacaacagtttcccaagatcctgaaactgagctctatactgtt  600


Query: 964  agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat  1023
            ||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Sbjct: 601  agcagcaaactggatttcaatatgacaaccaatcacagtttcatgtgtctcatcaagtat  660


Query: 1024 ggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcattttcct  1083
            ||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Sbjct: 661  ggacatttaagagtgaatcagaccttcaactggaacacacccaagcaagagcattttcct  720


Query: 1084 gataacctgctcccatcctgggccattaccttaatctcagtaaatggaatttttgtgata  1143
            ||||||||||||||||||||||||||||| | |||||||||||||||||||||||||||||
Sbjct: 721  gataacctgctcccatcctgggccattatcctaatctcagtaaatggaatttttgtgata  780


Query: 1144 tgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagagattg  1203
            |||||||||||||||||||| |||||||||| |||||||||||||| |||||||||| ||||
Sbjct: 781  tgctgcctgacctactgttttgccccaaggtgcagagagagaagaaggaatgagacattg  840


Query: 1204 agaagggaaagtgtacgccctgtat  1228
            |||||||||||||||||||||||||
Sbjct: 841  agaagggaaagtgtacgccctgtat  865
```


☐ >gi|13649996|gb|AF344839.1|AF344839   Cercocebus torquatus atys CD80 protein (MnB⁻
          Length = 867

  Score = 1501 bits (757), Expect = 0.0
  Identities = 838/865 (96%)
  Strand = Plus / Plus


```
Query: 364  atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttcttt  423
            |||||||||||||||||||||||||||| |||| |||||||||||||||||||| ||||||
Sbjct: 1    atgggccacacacggaggcagggaatatcatcatccaagtgtccatacctcaagttcttt  60


Query: 424  cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag  483
            ||||||||||||||||||||| ||||||| |||||||||||||||||||||||||||||||
Sbjct: 61   cagctcttggtgctggcttgtctttctcatttctgttcaggtgttatccacgtgaccaag  120


Query: 484  gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca  543
            ||||||||||||||||||||||||||||||||||||||||.|||||||||||||||||||||
Sbjct: 121  gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca  180


Query: 544  caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac  603
```

```
                |||||||||||||||||  |||||||||||||||||||||||||||||||||  ||||||||||
Sbjct:   181    caaactcgcatctactgccaaaaggagaagaaaatggtgctgactatgatatctggggac   240


Query:   604    atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc   663
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   241    atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc   300


Query:   664    attgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag   723
                ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   301    attgtgattctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag   360


Query:   724    tatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaagct   783
                ||||||||||  ||||||||||||·  |||||||||||||||||||||  ||||||  ||||||||||
Sbjct:   361    tatgaaaaagatgctttcaagcgagaacacctggctgaagtgatgttatccgtcaaagct   420


Query:   784    gacttccctacacctagtatatctgactttgaaattccaacttctaatattagaaggata   843
                ||||||||||||||||||||||||  ||||||||||||||||||  |||||||  ||||||||||||
Sbjct:   421    gacttccctacacctagtataactgactttgaaattccaccttctaacattagaaggata   480


Query:   844    atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa   903
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct:   481    atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagga   540


Query:   904    gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgtt   963
                |||||||||||||||  |||||||||||||||||||||||||||||||||||||||  |||||
Sbjct:   541    gaattaaatgccatcgacacaacagtttcccaagatcctgaaactgagctctatactgtt   600


Query:   964    agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat   1023
                ||||||||||||||||||||||||||||||||||  |||||  ||  |||||||||||||||||||
Sbjct:   601    agcagcaaactggatttcaatatgacaaccaatcacagttttgtgtgtctcatcaagtat   660


Query:   1024   ggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcattttcct   1083
                ||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Sbjct:   661    ggacatttaagagtgaatcagaccttcaactggaatacacccaagcaagagcattttcct   720


Query:   1084   gataacctgctcccatcctgggccattaccttaatctcagtaaatggaattttttgtgata   1143
                ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Sbjct:   721    gataacctgctcccatcctgggccattaccctaatctcagtaaatggaattttttgtgata   780


Query:   1144   tgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagagattg   1203
                |||||||||||||||||||||  ||||||||||||||||||||||||||  ||||||||||  ||||
Sbjct:   781    tgctgcctgacctactgttttgccccaagatgcagagagagaagaaggaatgagacattg   840


Query:   1204   agaagggaaagtgtacgccctgtat   1228
                |||||||||||||||||||||||||
Sbjct:   841    agaagggaaagtgtacgccctgtat   865
```

☐ >gi|644797|gb|U19840.1|MMU19840   Macaca mulatta B7 protein (B7) mRNA, complete cc
          Length = 867

 Score = 1501 bits (757), Expect = 0.0
 Identities = 838/865 (96%)
 Strand = Plus / Plus

Query: 364   atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttcttt 423
             |||||||||||||||||||||||| || |||||||||||||||||||||||| ||||||
Sbjct: 1   atgggccacacacggaggcaggaaatatcaccatccaagtgtccatacctcaagttcttt 60

Query: 424   cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag 483
             |||||||||||||||||| |||||||||| ||||||||||||||||||||||||||||||
Sbjct: 61   cagctcttggtgctggcttgtctttctcatttctgttcaggtgttatccacgtgaccaag 120

Query: 484   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 180

Query: 544   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 603
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 240

Query: 604   atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 663
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct: 241   atgaatatatggcccgagtacaagaaccggaccatctttgatatcacaaataacctctcc 300

Query: 664   attgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 723
             ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   attgtgattctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 360

Query: 724   tatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaagct 783
             |||||||||| |||||||||||||||||||||||||||||||| ||||| ||||||||||
Sbjct: 361   tatgaaaaagatgctttcaagcgggaacacctggctgaagtgatgttatccgtcaaagct 420

Query: 784   gacttccctacacctagtatatctgactttgaaattccaacttctaatattagaaggata 843
             |||||||||||||||||||| |||||| |||||||||||| ||||| |||||||||||||
Sbjct: 421   gacttccctacacctagtataactgactctgaaattccaccttctaacattagaaggata 480

Query: 844   atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa 903
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481   atttgctcaaactctggaggttttccagagcctcacctctcctggttggaaaatggagaa 540

Query: 904   gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgtt 963
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 541   gaattaaatgccatcagcacaacagtttcccaagatcctgaaactgagctctatactgtt 600

Query: 964   agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat 1023
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Sbjct: 601   agcagcaaactggatttcaatatgacaaccaatcacagtttcatgtgtctcatcaagtat 660


Query: 1024  ggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcattttcct 1083
             ||||||||||||||||||||||||||||||||||||||| |||  ||||||||||||||||
Sbjct: 661   ggacatttaagagtgaatcagaccttcaactggaacacacccaagcaagagcattttcct 720


Query: 1084  gataacctgctcccatcctgggccattaccttaatctcagtaaatggaattttttgtgata 1143
             |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||
Sbjct: 721   gataacctgctcccatcctgggccattatcctaatctcagtaaatggaattttttgtgata 780


Query: 1144  tgctgcctgacctactgctttgccccaagatgcagagagagaaggaggaatgagagattg 1203
             |||||||||||||||||| ||||||||| ||||||||||||||| |||||||||| ||||
Sbjct: 781   tgctgcctgacctactgtttttgccccaaggtgcagagagagaagaaggaatgagacattg 840


Query: 1204  agaagggaaagtgtacgccctgtat 1228
             |||||||||||||||||||||||||
Sbjct: 841   agaagggaaagtgtacgccctgtat 865
```

☐ >gi|644783|gb|U19833.1|CTU19833   Cercocebus torquatus B7 protein (B7) mRNA, parti
             Length = 868

 Score = 1501 bits (757), Expect = 0.0
 Identities = 838/865 (96%)
 Strand = Plus / Plus

```
Query: 364   atgggccacacacggaggcagggaacatcaccatccaagtgtccatacctcaatttcttt 423
             |||||||||||||||||||||||||||||| |||| ||||||||||||||||||| ||||||
Sbjct: 1     atgggccacacacggaggcagggaatatcatcatccaagtgtccatacctcaagttcttt 60


Query: 424   cagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaag 483
             |||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||||||
Sbjct: 61    cagctcttggtgctggcttgtctttctcattctgttcaggtgttatccacgtgaccaag 120


Query: 484   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 543
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   gaagtgaaagaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggca 180


Query: 544   caaactcgcatctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggac 603
             |||||||||||||||||| |||||||||||||||||||||||||||||||||| ||||||||
Sbjct: 181   caaactcgcatctactgccaaaaggagaagaaaatggtgctgactatgatatctggggac 240


Query: 604   atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 663
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   atgaatatatggcccgagtacaagaaccggaccatctttgatatcactaataacctctcc 300


Query: 664   attgtgatcctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 723
             ||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   attgtgattctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaag 360
```

```
Query:  724  tatgaaaaagacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaagct  783
             ||||||||||| |||||||||| |||||||||||||||||||||| |||||| ||||||||||
Sbjct:  361  tatgaaaaagatgctttcaagcgagaacacctggctgaagtgatgttatccgtcaaagct  420


Query:  784  gacttccctacacctagtatatctgactttgaaattccaacttctaatattagaaggata  843
             |||||||||||||||||||| |||||||||||||||||||| |||||| |||||||||||
Sbjct:  421  gacttccctacacctagtataactgactttgaaattccaccttctaacattagaaggata  480


Query:  844  atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagaa  903
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct:  481  atttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatggagga  540


Query:  904  gaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgtt  963
             ||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||
Sbjct:  541  gaattaaatgccatcgacacaacagtttcccaagatcctgaaactgagctctatactgtt  600


Query:  964  agcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaagtat 1023
             |||||||||||||||||||||||||||||||||||| ||||| || |||||||||||||||
Sbjct:  601  agcagcaaactggatttcaatatgacaaccaatcacagttttgtgtgtctcatcaagtat  660


Query: 1024  ggacatttaagagtgaatcagaccttcaactggaatacaaccaagcaagagcatttttcct 1083
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct:  661  ggacatttaagagtgaatcagaccttcaactggaatacacccaagcaagagcattttcct  720


Query: 1084  gataacctgctcccatcctgggccattaccttaatctcagtaaatggaattttttgtgata 1143
             ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct:  721  gataacctgctcccatcctgggccattaccctaatctcagtaaatggaattttttgtgata  780


Query: 1144  tgctgcctgacctactgctttgccccaagatgcagagagagagaaggaggaatgagagattg 1203
             ||||||||||||||||||||| ||||||||||||||||||||||||| ||||||||| ||||
Sbjct:  781  tgctgcctgacctactgttttgccccaagatgcagagagagaagaaggaatgagacattg  840


Query: 1204  agaagggaaagtgtacgccctgtat 1228
             |||||||||||||||||||||||||
Sbjct:  841  agaagggaaagtgtacgccctgtat 865
```

□ >gi|22651512|gb|AY081815.1| Ⓤ Homo sapiens costimulatory molecule variant IgV-CI
         complete cds, alternatively spliced
         Length = 736

```
 Score = 1027 bits (518), Expect = 0.0
 Identities = 528/530 (99%), Gaps = 1/530 (0%)
 Strand = Plus / Plus


Query:  252  cgtgagcaattggattgtcatcagccctgcctgttttgcacctgggaagtgccctggtct  311
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:    1  cgtgagcaattggattgtcatcagccctgcctgttttgcacctgggaagtgccctggtct  60
```

```
Query: 312  tacttgggtccaaattgttggctttcacttttgaccctaagcatctgaagccatgggcca  371
             ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   tac-tgggtccaaattgttggctttcacttttgaccctaagcatctgaagccatgggcca  119


Query: 372  cacacggaggcagggaacatcaccatccaagtgtccatacctcaatttctttcagctctt  431
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 120  cacacggaggcagggaacatcaccatccaagtgtccatacctcaatttctttcagctctt  179


Query: 432  ggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaaggaagtgaa  491
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 180  ggtgctggctggtctttctcacttctgttcaggtgttatccacgtgaccaaggaagtgaa  239


Query: 492  agaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggcacaaactcg  551
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 240  agaagtggcaacgctgtcctgtggtcacaatgtttctgttgaagagctggcacaaactcg  299


Query: 552  catctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatat  611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 300  catctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatat  359


Query: 612  atggcccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgat  671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 360  atggcccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgat  419


Query: 672  cctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaagtatgaaaa  731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct: 420  cctggctctgcgcccatctgacgagggcacatacgagtgtgttgttctgaagtctgaaaa  479


Query: 732  agacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaag  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 480  agacgctttcaagcgggaacacctggctgaagtgacgttatcagtcaaag  529
```

☐ >gi|179324|gb|M83073.1|HUMB7AN03   Homo sapiens antigen B7 gene, exon 3
            Length = 527

 Score = 634 bits (320), Expect = e-178
 Identities = 320/320 (100%)
 Strand = Plus / Plus

```
Query: 462  aggtgttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaa  521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 102  aggtgttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtggtcacaa  161


Query: 522  tgtttctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggt  581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 162  tgtttctgttgaagagctggcacaaactcgcatctactggcaaaaggagaagaaaatggt  221
```

```
Query: 582 gctgactatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctt 641
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 222 gctgactatgatgtctggggacatgaatatatggcccgagtacaagaaccggaccatctt 281


Query: 642 tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac 701
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 282 tgatatcactaataacctctccattgtgatcctggctctgcgcccatctgacgagggcac 341


Query: 702 atacgagtgtgttgttctgaagtatgaaaaagacgctttcaagcgggaacacctggctga 761
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 342 atacgagtgtgttgttctgaagtatgaaaaagacgctttcaagcgggaacacctggctga 401


Query: 762 agtgacgttatcagtcaaag 781
            ||||||||||||||||||||
Sbjct: 402 agtgacgttatcagtcaaag 421
```

☐ >gi|179323|gb|M83072.1|HUMB7AN02   Homo sapiens antigen B7 gene, exon 2
              Length = 521

 Score = 599 bits (302), Expect = e-167
 Identities = 302/302 (100%)
 Strand = Plus / Plus

```
Query: 164 gctgtgaaactaaatccacaacctttggagacccaggaacaccctccaatctctgtgtgt 223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 120 gctgtgaaactaaatccacaacctttggagacccaggaacaccctccaatctctgtgtgt 179


Query: 224 tttgtaaacatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcct 283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 180 tttgtaaacatcactggagggtcttctacgtgagcaattggattgtcatcagccctgcct 239


Query: 284 gttttgcacctgggaagtgccctggtcttacttgggtccaaattgttggctttcactttt 343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 240 gttttgcacctgggaagtgccctggtcttacttgggtccaaattgttggctttcactttt 299


Query: 344 gaccctaagcatctgaagccatgggccacacacggaggcagggaacatcaccatccaagt 403
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 300 gaccctaagcatctgaagccatgggccacacacggaggcagggaacatcaccatccaagt 359


Query: 404 gtccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcag 463
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 360 gtccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcag 419


Query: 464 gt 465
            ||
Sbjct: 420 gt 421
```

□ >gi|179325|gb|M83074.1|HUMB7AN04   Homo sapiens antigen B7 gene, exon 4
            Length = 510

 Score = 563 bits (284), Expect = e-157
 Identities = 284/284 (100%)
 Strand = Plus / Plus

Query: 780   agctgacttccctacacctagtatatctgactttgaaattccaacttctaatattagaag 839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   agctgacttccctacacctagtatatctgactttgaaattccaacttctaatattagaag 180

Query: 840   gataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatgg 899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   gataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaatgg 240

Query: 900   agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   agaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctctatgc 300

Query: 960   tgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 1019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   tgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcatcaa 360

Query: 1020 gtatggacatttaagagtgaatcagaccttcaactggaatacaa 1063
             ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361   gtatggacatttaagagtgaatcagaccttcaactggaatacaa 404

□ >gi|1262191|gb|U33208.1|HSU33208 G Human B-lymphocyte activation antigen (B7.1)
              and 5' UTR
            Length = 3921

 Score = 325 bits (164), Expect = 3e-85
 Identities = 164/164 (100%)
 Strand = Plus / Plus

Query: 1   aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3449 aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 3508

Query: 61   atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3509 atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 3568

Query: 121   aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 164
             ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3569 aaatcaaaggatttaaagaaaaagtggaatttttcttcagcaag 3612

☐ >gi|179322|gb|M83071.1|HUMB7AN01   Homo sapiens antigen B7 gene, exon 1
            Length = 374

Score = 325 bits (164), Expect = 3e-85
Identities = 164/164 (100%)
Strand = Plus / Plus

Query: 1   aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 110   aagtaacagaagttagaaggggaaatgtcgcctctctgaagattacccaaagaaaaagtg 169

Query: 61   atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 170   atttgtcattgctttatagactgtaagaagagaacatctcagaagtggagtcttaccctg 229

Query: 121   aaatcaaaggatttaaagaaaaagtggaattttcttcagcaag 164
             |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 230   aaatcaaaggatttaaagaaaaagtggaattttcttcagcaag 273

☐ >gi|46849851|gb|AY591920.1| Macaca fascicularis CD80 mRNA, partial cds
            Length = 184

Score = 317 bits (160), Expect = 7e-83
Identities = 178/184 (96%)
Strand = Plus / Plus

Query: 682   cgcccatctgacgagggcacatacgagtgtgttgttctgaagtatgaaaaagacgctttc 741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct: 1   cgcccatctgacgagggcacatacgagtgtgttgttctgaagtatgaaaaagatgctttc 60

Query: 742   aagcgggaacacctggctgaagtgacgttatcagtcaaagctgacttccctacacctagt 801
             |||||||||||||||||||||||||||| ||||||| |||||||||||||||||||||||
Sbjct: 61   aagcgggaacacctggctgaagtgatgttatccgtcaaagctgacttccctacacctagt 120

Query: 802   atatctgactttgaaattccaacttctaatattagaaggataatttgctcaacctctgga 861
             ||| ||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||
Sbjct: 121   ataactgactttgaaattccaccttctaacattagaaggataatttgctcaacctctgga 180

Query: 862   ggtt 865
             ||||
Sbjct: 181   ggtt 184

☐ >gi|2065520|gb|U57755.1|FCU57755   Felis catus T-cell specific surface glycoprotei
            cds
            Length = 941

Score = 254 bits (128), Expect = 9e-64

Identities = 221/252 (87%)
Strand = Plus / Plus

Query: 775   gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
             |||| |||||||||||||| ||||||||| |||| ||| || |||| || ||| ||
Sbjct: 412   gtcagagctgacttccctgtccctagtataactgatcttggaaatccatctcataacatc 471

Query: 835   agaaggataatttgctcaacctctggaggtttttccagagcctcacctctcctggttggaa 894
             | |||||||||| |||| ||| |||||||||||||||| |||||||||||||||||| |||||
Sbjct: 472   aaaaggataatgtgcttaacttctggaggtttttccaaagcctcacctctcctggctggaa 531

Query: 895   aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 532   aatgaagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 591

Query: 955   tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
             || || ||||||| ||||||||||||||||||||||||| |||||| |||||| |||||||
Sbjct: 592   tacactattagcagtgaactggatttcaatatgacaaacaaccatagcttcctgtgtctt 651

Query: 1015 atcaagtatgga 1026
             ||||||||||||
Sbjct: 652   gtcaagtatgga 663

 Score = 54.0 bits (27), Expect = 0.002
 Identities = 66/79 (83%)
 Strand = Plus / Plus

Query: 419   tctttcagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtga 478
             |||||| ||||||| |||| ||| ||||||| | ||||||||||||| | |||||| ||||
Sbjct: 56   tctttccgctcttgatgctagctagtcttttttacttctgttcaggtatcatccaggtga 115

Query: 479   ccaaggaagtgaaagaagt 497
             |||| |||| |||||||||
Sbjct: 116   acaagacagtggaagaagt 134

 Score = 50.1 bits (25), Expect = 0.026
 Identities = 31/33 (93%)
 Strand = Plus / Plus

Query: 653   ataacctctccattgtgatcctggctctgcgcc 685
             |||||| ||||||||||||| |||||||||||
Sbjct: 290   ataaccactccattgtgatcatggctctgcgcc 322

□ >gi|9796385|dbj|AB030651.1| Felis catus mRNA for B-lymphocyte activation antiger
                complete cds
          Length = 2718

```
Score =  254 bits (128), Expect = 9e-64
Identities = 221/252 (87%)
Strand = Plus / Plus


Query: 775   gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
             ||||  |||||||||||||     |||||||||| ||||   ||| || |||| ||   ||| ||
Sbjct: 620   gtcagagctgacttccctgtccctagtataactgatcttggaaatccatctcataacatc 679


Query: 835   agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894
             | ||||||||| |||| ||| |||||||||||||| |||||||||||||||||| |||||
Sbjct: 680   aaaaggataatgtgcttaacttctggaggttttccaaagcctcacctctcctggctggaa 739


Query: 895   aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
             ||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 740   aatgaagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 799


Query: 955   tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
             || || |||||||  |||||||||||||||||||||||| |||||| |||||| |||||||
Sbjct: 800   tacactattagcagtgaactggatttcaatatgacaaacaaccatagcttcctgtgtctt 859


Query: 1015  atcaagtatgga 1026
             |||||||||||
Sbjct: 860   gtcaagtatgga 871



Score =  155 bits (78), Expect = 6e-34
Identities = 125/138 (90%), Gaps = 2/138 (1%)
Strand = Plus / Plus


Query: 1991  actggttcatattggactgataatctctttaaatggctttatgctagtttgacctcattt 2050
             |||||||||||||||||||||||||||||| |||||||||| ||| | |||| ||||||||||
Sbjct: 1825  actggttcatattggactgataatctccttaaatggcttcatgtt-gtttaacctcattt 1883


Query: 2051  gtaaaatatttatgagaaagttctcatttaaaatgagatcgttgtttacagtgtatgtac 2110
             |||||||||||||||||||||||||||||||||||||||||| | | |||| |||||| |||
Sbjct: 1884  ataaaatatttatgagaaagttctcatttaaaatgagataggttttattgtgtat-tac 1942


Query: 2111  taagcagtaagctatctt 2128
             ||| ||||||||||||||
Sbjct: 1943  taaacagtaagctatctt 1960



Score = 69.9 bits (35), Expect = 3e-08
Identities = 56/63 (88%)
Strand = Plus / Plus


Query: 1528  ggaggtgacccgaattataaaggccagcgccagaacccagatttcctaactctggtgctc 1587
             ||||||||| |||| || |||||||| ||||||||||||||||||||    ||||||||||
```

```
Sbjct: 1374 ggaggtgacctgaatgatcaaggccagagccagaacccagatttcctgtgtctggtgctc 1433


Query: 1588 ttt 1590
             |||
Sbjct: 1434 ttt 1436



 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 102/125 (81%), Gaps = 1/125 (0%)
 Strand = Plus / Plus


Query: 1306 ttcctcagatggacaagattaccccaccttgccctttacgtatctgctct-taggtgctt 1364
             ||||||||||||| || ||||| |||||||||   ||| | |||||||| | | |||| || |
Sbjct: 1157 ttcctcagatggccaggattatcccaccttgtacttcatgtatctgttttctaggagcct 1216


Query: 1365 cttcacttcagttgctttgcaggaagtgtctagaggaatatggtgggcacagaagtagct 1424
             ||||| |||||| ||| |||||| ||||| |||| |||||| ||||| ||| ||||||||
Sbjct: 1217 cttcatttcagtggctctgcagaaagtgactagtggaatacagtgggaacattagtagct 1276


Query: 1425 ctggt 1429
             |||||
Sbjct: 1277 ctggt 1281



 Score = 56.0 bits (28), Expect = 4e-04
 Identities = 37/40 (92%)
 Strand = Plus / Plus


Query: 1898 ctatccaaaactaatttcctctgacatgtaagacgaatga 1937
             ||||||||||||||||| |||||| |||||||||| ||||||
Sbjct: 1735 ctatccaaaactaatatcctctaacatgtaagatgaatga 1774



 Score = 54.0 bits (27), Expect = 0.002
 Identities = 66/79 (83%)
 Strand = Plus / Plus


Query: 419 tctttcagctcttggtgctggctggtctttctcacttctgttcaggtgttatccacgtga 478
            |||||| |||||||| |||| ||| ||||||| | |||||||||||||| | |||||| ||||
Sbjct: 264 tctttccgctcttgatgctagctagtcttttttacttctgttcaggtatcatccaggtga 323


Query: 479 ccaaggaagtgaaagaagt 497
            |||| |||| |||||||||
Sbjct: 324 acaagacagtggaagaagt 342



 Score = 52.0 bits (26), Expect = 0.007
 Identities = 66/78 (84%), Gaps = 1/78 (1%)
 Strand = Plus / Plus
```

```
Query: 2150  ttccatagggcctccttagatccctaagatggcttttttctccttggtatttctgggtctt 2209
             |||||||||| |||| ||||| || |  |||||||| ||||||||| ||||||| |  || |
Sbjct: 1987  ttccatagggcttcctcagatcactgaagtggcttttcctccttggcatttct-gatcct  2045


Query: 2210  tctgacatcagcagagaa 2227
             |||||| |||||||||||
Sbjct: 2046  tctgagatcagcagagaa 2063



 Score = 50.1 bits (25), Expect = 0.026
 Identities = 31/33 (93%)
 Strand = Plus / Plus


Query: 653  ataacctctccattgtgatcctggctctgcgcc 685
            ||||||  ||||||||||||| ||||||||||||
Sbjct: 498  ataaccactccattgtgatcatggctctgcgcc 530
```

□ >gi|6653506|gb|AF203443.1|AF203443 **L U** Sus scrofa CD80 protein precursor (CD80)
            Length = 1167

 Score = 226 bits (114), Expect = 2e-55
 Identities = 240/282 (85%)
 Strand = Plus / Plus

```
Query: 775  gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
            ||||||||||||||| ||||    |||||||| ||| | ||| || |||| || |||| ||
Sbjct: 701  gtcaaagctgactttcctgtgcctagtattactgcccttggaaatccatctcctaacatc 760


Query: 835  agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894
            | |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 761  aaaaggataaggtgctcaacctctggaggttttccagagcctcacctctcctggttggaa 820


Query: 895  aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
            ||||||||||||||||||||| | |||||| |    |||||||||||||||||||||||||
Sbjct: 821  aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 880


Query: 955  tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
            ||     |||||||  ||||||||||||||| |||||  ||||||||||||||||||||||
Sbjct: 881  tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 940


Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
            |||||||||||  |||| ||||    |||||||||||||||||
Sbjct: 941  gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 982
```

 Score = 75.8 bits (38), Expect = 5e-10
 Identities = 107/130 (82%)

Strand = Plus / Plus

```
Query: 556  tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615
            |||||||||||||| ||  |||||||||||| || | |||||||||   | |||| | |||
Sbjct: 482  tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 541


Query: 616  cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675
            ||| ||||  ||||||| ||| ||  |||| |||| |||||||||| |||||||||||||||
Sbjct: 542  cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 601


Query: 676  gctctgcgcc 685
            ||||||||||
Sbjct: 602  gctctgcgcc 611
```

  Score = 67.9 bits (34), Expect = 1e-07
  Identities = 43/46 (93%)
  Strand = Plus / Plus

```
Query: 419  tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464
            |||||||||||||||||||||||| |||||||| | |||||||||||
Sbjct: 345  tctttcagctcttggtgctggttggtctttttgacttctgttcagg 390
```

  Score = 50.1 bits (25), Expect = 0.026
  Identities = 46/53 (86%)
  Strand = Plus / Plus

```
Query: 137  agaaaaagtggaattttttcttcagcaagctgtgaaactaaatccacaacccttt 189
            ||||||   |||||||| ||||||||||||| ||||||| |||||| |||| ||||
Sbjct: 57   agaaaaggaggaattattcttcagcaagttgtgaaaataaatctacaatcttt 109
```


□ >gi|6653504|gb|AF203442.1|AF203442 Ⓤ Sus scrofa CD80 protein precursor (CD80) mł
            Length = 1206

  Score = 226 bits (114), Expect = 2e-55
  Identities = 240/282 (85%)
  Strand = Plus / Plus

```
Query: 775  gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
            ||||||||||||| |||    |||||||| ||| | ||| || |||| || |||| ||
Sbjct: 701  gtcaaagctgactttcctgtgcctagtattactgcccttggaaatccatctcctaacatc 760


Query: 835  agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894
            | |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 761  aaaaggataaggtgctcaacctctggaggttttccagagcctcacctctcctggttggaa 820


Query: 895  aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
```

```
            ||||||||||||||||||||| | |||||| |    ||||||||||||||||||||||||||
Sbjct: 821  aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 880


Query: 955  tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
            ||      ||||||| |||||||||||||| |||||  |||||||||||||||||||||||
Sbjct: 881  tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 940


Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
            ||||||||||   |||| ||||   ||||||||||||||||||
Sbjct: 941  gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 982



 Score = 75.8 bits (38), Expect = 5e-10
 Identities = 107/130 (82%)
 Strand = Plus / Plus


Query: 556  tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615
            |||||||||||| || ||||||||||||| || | |||||||   |  |||| | | |||
Sbjct: 482  tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 541


Query: 616  cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675
            ||| ||||  |||||||| ||| ||  |||| |||| ||||||||| |||||||||||||
Sbjct: 542  cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 601


Query: 676  gctctgcgcc 685
            ||||||||||
Sbjct: 602  gctctgcgcc 611



 Score = 67.9 bits (34), Expect = 1e-07
 Identities = 43/46 (93%)
 Strand = Plus / Plus


Query: 419  tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464
            |||||||||||||||||||||||| ||||||| | ||||||||||||
Sbjct: 345  tctttcagctcttggtgctggttggtctttttgacttctgttcagg 390



 Score = 50.1 bits (25), Expect = 0.026
 Identities = 46/53 (86%)
 Strand = Plus / Plus


Query: 137  agaaaaagtggaattttttcttcagcaagctgtgaaactaaatccacaaccttt 189
            |||||| | ||||||| |||||||||||| ||||||| |||||| |||| ||||
Sbjct: 57   agaaaaggaggaattattcttcagcaagttgtgaaaataaatctacaatcttt 109
```

☐ >gi|18072036|gb|AF455811.1| **L U** Sus scrofa CD80 (CD80) mRNA, complete cds
         Length = 1112

Score = 226 bits (114), Expect = 2e-55
Identities = 240/282 (85%)
Strand = Plus / Plus


```
Query: 775   gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
             |||||||||||||| |||    ||||||||| |||  | ||| || ||||  || |||| ||
Sbjct: 397   gtcaaagctgactttcctgtgcctagtattactgcccttggaaatccatctcctaacatc 456


Query: 835   agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894
             |  |||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 457   aaaaggataaggtgctcaacctctggaggttttccagagcctcacctctcctggttggaa 516


Query: 895   aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
             |||||||||||||||||||| | |||||| |     ||||||||||||||||||||||||||
Sbjct: 517   aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 576


Query: 955   tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
             ||      |||||||  |||||||||||||| |||||   |||||||||||||||||||||
Sbjct: 577   tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 636


Query: 1015  atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
             |||||||||||   |||| ||||    ||||||||||||||||
Sbjct: 637   gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 678
```


Score = 75.8 bits (38), Expect = 5e-10
Identities = 107/130 (82%)
Strand = Plus / Plus


```
Query: 556   tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615
             ||||||||||||| ||  |||||||||||| ||| || | ||||||||   |||| | |||
Sbjct: 178   tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 237


Query: 616   cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675
             ||| |||| |||||||||| |||| || || |||| |||| |||||||||| ||||||||||
Sbjct: 238   cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 297


Query: 676   gctctgcgcc 685
             ||||||||||
Sbjct: 298   gctctgcgcc 307
```


Score = 60.0 bits (30), Expect = 3e-05
Identities = 42/46 (91%)
Strand = Plus / Plus


```
Query: 419   tctttcagctcttggtgctggctggtcttctcacttctgttcagg 464
             |||||||||||||||||||| || |||||||| | ||||||||||||
```

Sbjct: 41   tctttcagctcttggtgccggttggtcttttgacttctgttcagg 86

□ >gi|8100070|dbj|AB038153.2| U Sus scrofa mRNA for CD80 protein precursor, comple
          Length = 1220

 Score = 226 bits (114), Expect = 2e-55
 Identities = 240/282 (85%)
 Strand = Plus / Plus

Query: 775   gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
             ||||||||||||||| ||| ||||||||| ||| | ||| || |||| || |||| ||
Sbjct: 716   gtcaaagctgactttcctgtgcctagtattactgcccttggaaatccatctcctaacatc 775

Query: 835   agaaggataatttgctcaacctctggaggtttttccagagcctcacctctcctggttggaa 894
             | ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 776   aaaaggataaggtgctcaacctctggaggttttccagagcctcacctctcctggttggaa 835

Query: 895   aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
             |||||||||||||||||||| | |||||| | ||||||||||||||||||||||||||
Sbjct: 836   aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 895

Query: 955   tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
             || ||||||| |||||||||||||||| ||||| |||||||||||||||||||
Sbjct: 896   tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 955

Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
             |||||||||| |||| |||| |||||||||||||||||
Sbjct: 956   gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 997

 Score = 75.8 bits (38), Expect = 5e-10
 Identities = 107/130 (82%)
 Strand = Plus / Plus

Query: 556   tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615
             |||||||||||||| || |||||||||||| || | |||||||| | |||| | |||
Sbjct: 497   tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 556

Query: 616   cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675
             ||| |||| |||||||| ||| || |||| |||| |||||||||||||| |||||||||||
Sbjct: 557   cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 616

Query: 676   gctctgcgcc 685
             ||||||||||
Sbjct: 617   gctctgcgcc 626

 Score = 67.9 bits (34), Expect = 1e-07

```
Identities = 43/46 (93%)
Strand = Plus / Plus


Query: 419 tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464
            |||||||||||||||||||||||| ||||||||| | ||||||||||
Sbjct: 360 tctttcagctcttggtgctggttggtctttttgacttctgttcagg 405



Score = 42.1 bits (21), Expect = 6.4
Identities = 45/53 (84%)
Strand = Plus / Plus


Query: 137 agaaaaagtggaattttttcttcagcaagctgtgaaactaaatccacaacctttt 189
            ||||||  | ||||||| ||||||||||||| | ||||| |||||| |||| ||||
Sbjct: 72  agaaaaggaggaattattcttcagcaagttatgaaaataaatctacaatcttt 124
```

☐ >gi|13591561|dbj|AB049760.1| 🄻🄾 Sus scrofa CD80/B7-1 mRNA for CD80 protein prec
            Length = 2710

```
Score =  226 bits (114), Expect = 2e-55
Identities = 240/282 (85%)
Strand = Plus / Plus


Query: 775  gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
            ||||||||||||| |||    ||||||||| ||| | ||| || |||| || |||| ||
Sbjct: 716  gtcaaagctgactttcctgtgcctagtattactgcccttggaaatccatctcctaacatc 775


Query: 835  agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894
            | |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 776  aaaaggataaggtgctcaacctctggaggtttttccagagcctcacctctcctggttggaa 835


Query: 895  aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
            |||||||||||||||||||||| | ||||||| |         |||||||||||||||||
Sbjct: 836  aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 895


Query: 955  tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
            ||          ||||||| |||||||||||| ||||| ||||||||||||||||||||||
Sbjct: 896  tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 955


Query: 1015 atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
            |||||||||| ||||  |||| ||||||||||||||||
Sbjct: 956  gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 997



Score = 75.8 bits (38), Expect = 5e-10
Identities = 107/130 (82%)
Strand = Plus / Plus
```

```
Query: 556  tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615
             |||||||||||||| ||  |||||||||| || | ||||||| · |  |||| | |||
Sbjct: 497  tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 556


Query: 616  cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675
             ||| |||| |||||||| ||| ||  |||| |||| ||||||||||| ||||||||||||
Sbjct: 557  cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 616


Query: 676  gctctgcgcc 685
             ||||||||||
Sbjct: 617  gctctgcgcc 626



 Score = 67.9 bits (34), Expect = 1e-07
 Identities = 43/46 (93%)
 Strand = Plus / Plus


Query: 419  tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464
             |||||||||||||||||||||||| |||||||| | ||||||||||||
Sbjct: 360  tctttcagctcttggtgctggttggtctttttgacttctgttcagg 405



 Score = 42.1 bits (21), Expect = 6.4
 Identities = 45/53 (84%)
 Strand = Plus / Plus


Query: 137  agaaaaagtggaattttttcttcagcaagctgtgaaactaaatccacaaccttt 189
             |||||| | |||||| |||||||||||| | ||||| |||||| |||| ||||
Sbjct: 72   agaaaaggaggaattattcttcagcaagttatgaaaataaatctacaatcttt 124



☐>gi|8100061|dbj|AB026121.2|  Ⓤ Sus scrofa mRNA for CD80 protein precursor, comple
          Length = 1189

 Score =  226 bits (114), Expect = 2e-55
 Identities = 240/282 (85%)
 Strand = Plus / Plus


Query: 775  gtcaaagctgacttccctacacctagtatatctgactttgaaattccaacttctaatatt 834
             ||||||||||||||| |||    |||||||| ||| | ||| || |||| || |||| ||
Sbjct: 716  gtcaaagctgactttcctgtgcctagtattactgcccttggaaatccatctcctaacatc 775


Query: 835  agaaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaa 894
             | |||||||   |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 776  aaaaggataaggtgctcaacctctggaggttttccagagcctcacctctcctggttggaa 835


Query: 895  aatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctc 954
             |||||||||||||||||||||| | |||||| |   ||||||||||||||||||||||||||
Sbjct: 836  aatggagaagaattaaatgctaccaacacgatgctttcccaagatcctgaaactgagctc 895
```

```
Query: 955   tatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctc 1014
              ||   |||||||  |||||||||||||| |||||  ||||||||||||||||||||||||||
Sbjct: 896   tacatgattagcagtgaactggatttcaatgtgacaggcaaccacagcttcatgtgtctt 955


Query: 1015  atcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
              ||||||||||||    |||| ||||    ||||||||||||||
Sbjct: 956   gtcaagtatggaggcttaacagtgtcacagaccttcaactgg 997



 Score = 75.8 bits (38), Expect = 5e-10
 Identities = 107/130 (82%)
 Strand = Plus / Plus


Query: 556   tactggcaaaaggagaagaaaatggtgctgactatgatgtctggggacatgaatatatgg 615
             |||||||||||||| ||  |||||||||||| || | ||||||||   | |||| | |||
Sbjct: 497   tactggcaaaaggataatgaaatggtgctggctgtcatgtctggaaaagtgaaggtgtgg 556


Query: 616   cccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatcctg 675
             ||| ||||  ||||||| ||| ||  | || |  |||| |||| ||||||||| |||||||
Sbjct: 557   cccaagtatgagaaccgcaccttcactgatgtcaccaataacctctgcattgtgatcctg 616


Query: 676   gctctgcgcc 685
             ||||||||||
Sbjct: 617   gctctgcgcc 626



 Score = 67.9 bits (34), Expect = 1e-07
 Identities = 43/46 (93%)
 Strand = Plus / Plus


Query: 419   tctttcagctcttggtgctggctggtctttctcacttctgttcagg 464
             |||||||||||||||||||||||| ||||||| | ||||||||||||
Sbjct: 360   tctttcagctcttggtgctggttggtctttttgacttctgttcagg 405



 Score = 42.1 bits (21), Expect = 6.4
 Identities = 45/53 (84%)
 Strand = Plus / Plus


Query: 137   agaaaaagtggaattttttcttcagcaagctgtgaaactaaatccacaaccttt 189
             ||||||  | |||||| |||||||||||| | |||||| |||||| |||| ||||
Sbjct: 72    agaaaaggaggaattattcttcagcaagttatgaaaataaatctacaatcttt 124



 ☐ >gi|179327|gb|M83077.1|HUMB7AN06  🅛 Homo sapiens antigen B7 gene, exon 6
             Length = 610

 Score =  220 bits (111), Expect = 1e-53
 Identities = 111/111 (100%)
```

Strand = Plus / Plus

Query: 1160 gctttgccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 1219
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 122   gctttgccccaagatgcagagagagaaggaggaatgagagattgagaagggaaagtgtac 181

Query: 1220 gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 1270
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 182   gccctgtataacagtgtccgcagaagcaaggggctgaaaagatctgaaggt 232

>gi|22775283|gb|AF536987.1| Synthetic construct CD28 binding protein precursor
                    complete cds
              Length = 912

 Score = 216 bits (109), Expect = 2e-52
 Identities = 172/193 (89%)
 Strand = Plus / Plus

Query: 827   ctaatattagaaggataatttgctcaacctctggaggttttccagagcctcacctctcct 886
              ||||||| |||||| ||||||||||||||||||||||||||||| ||| |||||||| ||
Sbjct: 473   ctaatatcagaaggctaatttgctcaacctctggaggttttccaaggccccacctctact 532

Query: 887   ggttggaaaatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaa 946
              |||||||||||||||||||||||||||| | ||||||||||||||||||||||||||| ||
Sbjct: 533   ggttggaaaatggagaagaattaaatgctaccaacacaacagtttcccaagatcctggaa 592

Query: 947   ctgagctctatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttca 1006
              |||||||||| ||||||| |||||||||||||| ||||||| |||||||||| ||
Sbjct: 593   ctgagctctacatgattagcagtgaactggatttcaatgtgacaaataaccacagcatcg 652

Query: 1007 tgtgtctcatcaa 1019
              |||||||||||||
Sbjct: 653   tgtgtctcatcaa 665

 Score = 52.0 bits (26), Expect = 0.007
 Identities = 38/42 (90%)
 Strand = Plus / Plus

Query: 423   tcagctcttggtgctggctggtctttctcacttctgttcagg 464
              |||||||||||||||| ||||||||| | |||||||||||||
Sbjct: 60   tcagctcttggtgctcactggtctttttacttctgttcagg 101

 Score = 46.1 bits (23), Expect = 0.41
 Identities = 23/23 (100%)
 Strand = Plus / Plus

```
Query: 664  attgtgatcctggctctgcgccc 686
            |||||||||||||||||||||||
Sbjct: 307  attgtgatcctggctctgcgccc 329
```

☐ >gi|2677623|emb|Y09950.1|BTCD80 L U B.taurus CD80 mRNA
              Length = 888

Score = 202 bits (102), Expect = 3e-48
Identities = 198/230 (86%)
Strand = Plus / Plus

```
Query: 827   ctaatattagaaggataatttgctcaacctctggaggttttccagagcctcacctctcct 886
             ||||||| |||||| ||||||||||||||||||||||||||||| ||| |||||||| ||
Sbjct: 473   ctaatatcagaaggctaatttgctcaacctctggaggttttccaaggccccacctctact 532


Query: 887   ggttggaaaatggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaa 946
             ||||||||||||||||||||||||||||| | |||||||||| | ||||||||||||||||
Sbjct: 533   ggttggaaaatggagaagaattaaatgctaccaacacaacactgtcccaagatcctgaaa 592


Query: 947   ctgagctctatgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttca 1006
             |  |||||||    ||||||| ||||||||||||| ||||||| ||| ||| ||||||||
Sbjct: 593   ccaagctctacatgattagcagtgaactggatttcaacatgacaagcaatcacagcttct 652


Query: 1007  tgtgtctcatcaagtatggacatttaagagtgaatcagaccttcaactgg 1056
             |||||| ||||||||||||| | |||| |||| |||||||||| |||||
Sbjct: 653   tgtgtcttgtcaagtatggagacttaacagtgtcacagaccttctactgg 702
```

Score = 52.0 bits (26), Expect = 0.007
Identities = 38/42 (90%)
Strand = Plus / Plus

```
Query: 423  tcagctcttggtgctggctggtctttctcacttctgttcagg 464
            ||||||||||||||| |||||||||| | ||||||||||||||
Sbjct: 60   tcagctcttggtgctcactggtcttttttacttctgttcagg 101
```

Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus

```
Query: 663  cattgtgatcctggctctgcgcc 685
            |||||||||||||||||||||||
Sbjct: 306  cattgtgatcctggctctgcgcc 328
```

☐ >gi|1685044|gb|U72535.1|HSU72535 L Homo sapiens LIM domain protein CRP2 (CSRP2P)
              B-lymphocyte activation antigen B7 gene, partial cds, and

```
                    exon 5
                Length = 2350

 Score =  192 bits (97), Expect = 3e-45
 Identities = 97/97 (100%)
 Strand = Plus / Plus


Query: 1064  ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag  1123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1835  ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag  1894


Query: 1124  taaatggaattttttgtgatatgctgcctgacctactg  1160
             |||||||||||||||||||||||||||||||||||||
Sbjct: 1895  taaatggaattttttgtgatatgctgcctgacctactg  1931
```

☐ >gi|179326|gb|M83075.1|HUMB7AN05   Homo sapiens antigen B7 gene, exon 5
            Length = 314

```
 Score =  192 bits (97), Expect = 3e-45
 Identities = 97/97 (100%)
 Strand = Plus / Plus


Query: 1064  ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag  1123
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 111   ccaagcaagagcattttcctgataacctgctcccatcctgggccattaccttaatctcag  170


Query: 1124  taaatggaattttttgtgatatgctgcctgacctactg  1160
             |||||||||||||||||||||||||||||||||||||
Sbjct: 171   taaatggaattttttgtgatatgctgcctgacctactg  207
```

☐ >gi|7739770|gb|AF257653.1|AF257653 Ⓤ Canis familiaris T-cell co-stimulatory prot
            complete cds
            Length = 972

```
 Score =  163 bits (82), Expect = 3e-36
 Identities = 163/190 (85%)
 Strand = Plus / Plus


Query: 837  aaggataaatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaa  896
            ||||||||| || |||||||||||||||||||||| ||||||||||||||||| ||||||
Sbjct: 500  aaggataatgtgttcaacctctggaggttttccaaagcctcacctctcctggtgggaaaa  559


Query: 897  tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta  956
            || ||||||||| |||||       |||||||||||||||||| || || ||||| | ||
Sbjct: 560  tgaagaagaattgaatgctgccaacacaacagtttcccaagacccggacactgagttgta  619


Query: 957  tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat  1016
            || |||| || ||||||||||||||||| |||| |||||| |||||    |||||||  |
```

```
Sbjct: 620   cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtcttgt  679


Query: 1017  caagtatgga  1026
             ||||||||||
Sbjct: 680   caagtatgga  689



 Score = 58.0 bits (29),  Expect = 1e-04
 Identities = 89/109 (81%)
 Strand = Plus / Plus


Query: 406   ccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggt  465
             |||||  |||||   |||  ||||||||||||||  |||  ||||  | |  |||||||||||||
Sbjct: 69    ccatatctcaaggtctctcagctcttggtgctagctagtctcttttacttctgttcaggc  128


Query: 466   gttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtg  514
             |  ||||| ||||  ||||   |||||||||||| |||   ||||||||||
Sbjct: 129   atcatccaggtgaacaagacagtgaaagaagtagcagtactgtcctgtg  177



 Score = 46.1 bits (23),  Expect = 0.41
 Identities = 35/39 (89%)
 Strand = Plus / Plus


Query: 647   tcactaataacctctccattgtgatcctggctctgcgcc  685
             ||||  ||||||||||||  |||||   ||||||||||||
Sbjct: 310   tcaccaataacctctccatcgtgattatggctctgcgcc  348




[ ] >gi|6572505|gb|AF106831.1|CFCD80Y4   Canis familiaris secreted B7-1 protein (CD80)
          spliced exon 4 and complete cds
          Length = 1130

 Score =  163 bits (82),  Expect = 3e-36
 Identities = 163/190 (85%)
 Strand = Plus / Plus


Query: 837   aaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaa  896
             ||||||||| ||  ||||||||||||||||||||| |||||||||||||||||||| ||||||
Sbjct: 262   aaggataatgtgttcaacctctggaggttttccaaagcctcacctctcctggtgggaaaa  321


Query: 897   tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta  956
             || |||||||||| |||||   |||||||||||||||||||||  || || |||||| | ||
Sbjct: 322   tgaagaagaattgaatgctgccaacacaacagtttcccaagacccggacactgagttgta  381


Query: 957   tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat  1016
             || ||||| ||  |||||||||||||||||||| |||| |||||| |||||  ||||||| |
Sbjct: 382   cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtcttgt  441
```

```
Query: 1017 caagtatgga 1026
             ||||||||||
Sbjct: 442  caagtatgga 451
```

>gi|6572514|gb|AF106825.1|AF106825 U Canis familiaris secreted B7-1 protein prec
            complete cds
          Length = 1024

 Score = 163 bits (82), Expect = 3e-36
 Identities = 163/190 (85%)
 Strand = Plus / Plus

```
Query: 837  aaggataatttgctcaacctctggaggtttttccagagcctcacctctcctggttggaaaa 896
            ||||||||| ||  ||||||||||||||||||| ||||||||||||||||||||| ||||||
Sbjct: 552  aaggataatgtgttcaacctctggaggtttttccaaagcctcacctctcctggtgggaaaa 611


Query: 897  tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956
            || |||||||||| ||||| ||||||||||||||||||||||||| || || ||||||| | ||
Sbjct: 612  tgaagaagaattgaatgctgccaacacaacagtttcccaagacccggacactgagttgta 671


Query: 957  tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat 1016
             || ||||| || ||||||||||||||||||| |||| ||||||| |||||| ||||||| |
Sbjct: 672  cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtcttgt 731


Query: 1017 caagtatgga 1026
             ||||||||||
Sbjct: 732  caagtatgga 741
```

 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 89/109 (81%)
 Strand = Plus / Plus

```
Query: 406  ccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggt 465
            ||||| |||||   ||| ||||||||||||||||| ||| |||| | | ||||||||||||
Sbjct: 121  ccatatctcaaggtctctcagctcttggtgctagctagtctcttttacttctgttcaggc 180


Query: 466  gttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtg 514
            | ||||| |||| |||| ||||||||||| |||      |||||||||||
Sbjct: 181  atcatccaggtgaacaagacagtgaaagaagtagcagtactgtcctgtg 229
```

 Score = 46.1 bits (23), Expect = 0.41
 Identities = 35/39 (89%)
 Strand = Plus / Plus

```
Query: 647  tcactaataacctctccattgtgatcctggctctgcgcc 685
            |||| ||||||||||||||| |||||   |||||||||||
Sbjct: 362  tcaccaataacctctccatcgtgattatggctctgcgcc 400
```

☐ >gi|6572512|gb|AF106824.1|AF106824   **L** **U** Canis familiaris B7-1 protein precursor ·
         Length = 2830

 Score = 163 bits (82), Expect = 3e-36
 Identities = 163/190 (85%)
 Strand = Plus / Plus

Query: 837   aaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaa 896
          |||||||||| || |||||||||||||||||||||||| |||||||||||||||| ||||||
Sbjct: 810   aaggataatgtgttcaacctctggaggttttccaaagcctcacctctcctggtgggaaaa 869

Query: 897   tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956
          || ||||||||| |||||| |||||||||||||||||||||||| || || |||||| | ||
Sbjct: 870   tgaagaagaattgaatgctgccaacacaacagtttcccaagacccggacactgagttgta 929

Query: 957   tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat 1016
           || |||| || |||||||||||||||| |||| |||||| |||||| ||||||| |
Sbjct: 930   cactattagtagtgaactggatttcaatataacaagcaaccatagctttgtgtgtcttgt 989

Query: 1017 caagtatgga 1026
           ||||||||||
Sbjct: 990 caagtatgga 999

 Score = 107 bits (54), Expect = 1e-19
 Identities = 89/99 (89%), Gaps = 5/99 (5%)
 Strand = Plus / Plus

Query: 1991 actggttcatattggactgataatctctttaaatggctttatgctagtttgacctcattt 2050
          |||||||||||||||||||||||||||| || |||||||||||||||||||| | |||||||
Sbjct: 1986 actggttcatattggactgataatctcctt-aatggctttatgctagtttaaactcattt 2044

Query: 2051 gtaaaatatttatgagaaagttctcatttaaaatgagat 2089
          ||||| |||||||||||||||||||||||||||||||||
Sbjct: 2045 ataaaa----catgagaaagttctcatttaaaatgagat 2079

 Score = 77.8 bits (39), Expect = 1e-10
 Identities = 136/167 (81%), Gaps = 1/167 (0%)
 Strand = Plus / Plus

Query: 1261 atctgaaggtctcacctccatttgcaattgacctcttctgggaacttcctcagatggaca 1320
          ||||| |||||| ||||||||| | ||||||||| ||| ||| |||||||||||| ||
Sbjct: 1259 atctggaggtcccacctccatcttagattgacctcatctttgaatttcctcagatggcca 1318

Query: 1321 agattaccccaccttgccctttacgtatctgctct-taggtgcttcttcacttcagttgc 1379
          ||||| |||||||||| ||| | | ||||| ||| |||| || | |||| |||||| ||

```
Sbjct: 1319 ggattatcccaccttgcacttcatgcatctgttctctaggagcctgttcatttcagtggc 1378


Query: 1380 tttgcaggaagtgtctagaggaatatggtgggcacagaagtagctct 1426
            |||||| |||||| | |||||||||||||||||| ||| |||||||||
Sbjct: 1379 cctgcagaaagtgaccagaggaatatggtggggacataagtagctct 1425



 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 89/109 (81%)
 Strand = Plus / Plus


Query: 406 ccatacctcaatttctttcagctcttggtgctggctggtctttctcacttctgttcaggt 465
           ||||| |||||  |||  ||||||||||||||||| ||| |||| | | ||||||||||||
Sbjct: 379 ccatatctcaaggtctctcagctcttggtgctagctagtctcttttacttctgttcaggc 438


Query: 466 gttatccacgtgaccaaggaagtgaaagaagtggcaacgctgtcctgtg 514
           | |||||| |||| |||| ||||||||||| |||    |||||||||||
Sbjct: 439 atcatccaggtgaacaagacagtgaaagaagtagcagtactgtcctgtg 487



 Score = 56.0 bits (28), Expect = 4e-04
 Identities = 58/68 (85%)
 Strand = Plus / Plus


Query: 1887 agaaaggagaactatccaaaactaatttcctctgacatgtaagacgaatgatttaggtac 1946
            |||||| ||| ||||||||||||||| || |||||||||||||| ||||||| ||| |||
Sbjct: 1871 agaaagtagatctatccaaaactaatatctgctgacatgtaagatgaatgacttatatac 1930


Query: 1947 gtcaaagc 1954
            |||||||
Sbjct: 1931 ctcaaagc 1938



 Score = 48.1 bits (24), Expect = 0.10
 Identities = 37/40 (92%), Gaps = 1/40 (2%)
 Strand = Plus / Plus


Query: 2188 ctccttggtatttctgggtctttctgacatcagcagagaa 2227
            |||||||||||||||||  | | |||||||||||||||||
Sbjct: 2199 ctccttggtatttctga-tccttctgacatcagcagagaa 2237



 Score = 48.1 bits (24), Expect = 0.10
 Identities = 51/60 (85%)
 Strand = Plus / Plus


Query: 1531 ggtgacccgaattataaaggccagcgccagaacccagatttcctaactctggtgctcttt 1590
            |||||||| ||||| |||||||| | | || |||||||||||||||||| ||| |||||||
Sbjct: 1518 ggtgacctgaatgataaaggtctgagctagaacccagatttcctgtctcgggtgctcttt 1577
```

```
 Score = 46.1 bits (23), Expect = 0.41
 Identities = 35/39 (89%)
 Strand = Plus / Plus


Query: 647 tcactaataacctctccattgtgatcctggctctgcgcc 685
           ||||  |||||||||||||| |||||  ||||||||||||
Sbjct: 620 tcaccaataacctctccatcgtgattatggctctgcgcc 658



 Score = 42.1 bits (21), Expect = 6.4
 Identities = 27/29 (93%)
 Strand = Plus / Plus


Query: 1670 tgtccaataacaggtcaacttcagagact 1698
            ||||||||  |||||||||||||||||||
Sbjct: 1659 tgtccaatgtcaggtcaacttcagagact 1687
```

☐ >gi|25188155|dbj|AB085743.1| Mesocricetus auratus B7-1b mRNA for B7-1, complete
          Length = 2071

```
 Score =  123 bits (62), Expect = 2e-24
 Identities = 125/146 (85%)
 Strand = Plus / Plus


Query: 856  tctggaggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgcc 915
            |||||||||||| ||||||||| |  | ||||||||||||| ||||| |||||||||| | |
Sbjct: 785  tctggaggtttcccagagcctcgcctcacctggttggaagatggaaaagaattaagcggc 844


Query: 916  atcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagcaaactg 975
            ||||| ||||||| |||| || || ||||||||| |||| || || |||| || |||||||
Sbjct: 845  atcaatacaacaatttctcaggatcctgaatctgaactgtacactgtcagtagcaaactg 904


Query: 976  gatttcaatatgacaaccaaccacag 1001
            |||||||||||||||  |||||||||
Sbjct: 905  gatttcaatatgacatacaaccacag 930



 Score = 48.1 bits (24), Expect = 0.10
 Identities = 45/52 (86%)
 Strand = Plus / Plus


Query: 553 atctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggaca 604
           |||||||||||||| ||  ||| |||||||||||| |  |  ||  ||||||||
Sbjct: 482 atctactggcaaaaagataaggaaatggtgctgagtttcatctctggggaca 533
```

Score = 44.1 bits (22), Expect = 1.6
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1262 tctgaaggtctcacctccatttgcaa 1287
             |||||||||||||||| ||||||||||
Sbjct: 1170 tctgaaggtctcacctacatttgcaa 1195

☐ >gi|25188153|dbj|AB085742.1| Mesocricetus auratus B7-1a mRNA for B7-1, complete
              Length = 3096

 Score = 123 bits (62), Expect = 2e-24
 Identities = 125/146 (85%)
 Strand = Plus / Plus

Query: 856   tctggaggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgcc 915
             |||||||||| ||||||||||| |||| |||||||||| ||||| ||||||||| | |
Sbjct: 786   tctggaggtttcccagagcctcgcctcacctggttggaagatggaaaagaattaagcggc 845

Query: 916   atcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagcaaactg 975
             ||||| |||||| |||| || || |||||||||| |||| || || |||| || |||||||||
Sbjct: 846   atcaatacaacaatttctcaggatcctgaatctgaactgtacactgtcagtagcaaactg 905

Query: 976   gatttcaatatgacaaccaaccacag 1001
             ||||||||||||||| |||||||||
Sbjct: 906   gatttcaatatgacatacaaccacag 931

 Score = 52.0 bits (26), Expect = 0.007
 Identities = 26/26 (100%)
 Strand = Plus / Plus

Query: 2063 tgagaaagttctcatttaaaatgaga 2088
             ||||||||||||||||||||||||||
Sbjct: 2257 tgagaaagttctcatttaaaatgaga 2282

 Score = 48.1 bits (24), Expect = 0.10
 Identities = 45/52 (86%)
 Strand = Plus / Plus

Query: 553   atctactggcaaaaggagaagaaaatggtgctgactatgatgtctggggaca 604
             |||||||||||||| || ||| |||||||||||| | | || ||||||||||
Sbjct: 483   atctactggcaaaaagataaggaaatggtgctgagtttcatctctggggaca 534

 Score = 44.1 bits (22), Expect = 1.6
 Identities = 25/26 (96%)
 Strand = Plus / Plus

```
Query: 1262 tctgaaggtctcacctccatttgcaa 1287
            |||||||||||||||| |||||||||
Sbjct: 1171 tctgaaggtctcacctacatttgcaa 1196
```

☐ >gi|6572508|gb|AF106834.1|CFCD80Y7 G Canis familiaris B7-1 protein (CD80) gene,
           Length = 2242

 Score = 107 bits (54), Expect = 1e-19
 Identities = 89/99 (89%), Gaps = 5/99 (5%)
 Strand = Plus / Plus

```
Query: 1991 actggttcatattggactgataatctctttaaatggctttatgctagtttgacctcattt 2050
            |||||||||||||||||||||||||||||| || |||||||||||||||||| | |||||||
Sbjct: 1092 actggttcatattggactgataatctcctt-aatggctttatgctagtttaaactcattt 1150
```

```
Query: 2051 gtaaaatatttatgagaaagttctcatttaaaatgagat 2089
            |||||       |||||||||||||||||||||||||||||
Sbjct: 1151 ataaaa----catgagaaagttctcatttaaaatgagat 1185
```

 Score = 73.8 bits (37), Expect = 2e-09
 Identities = 116/141 (82%), Gaps = 1/141 (0%)
 Strand = Plus / Plus

```
Query: 1287 attgacctcttctgggaacttcctcagatggacaagattacccaccttgccctttacgt 1346
            ||||||||| |||   ||| |||||||||||| || ||||| |||||||||| ||| | |
Sbjct: 391  attgacctcatctttgaatttcctcagatggccaggattatcccaccttgcacttcatgc 450
```

```
Query: 1347 atctgctct-taggtgcttcttcacttcagttgctttgcaggaagtgtctagaggaatat 1405
            ||||| ||| |||| || | |||| |||||| || ||||| ||||| | |||||||||
Sbjct: 451  atctgttctctaggagcctgttcatttcagtggccctgcagaaagtgaccagaggaatat 510
```

```
Query: 1406 ggtgggcacagaagtagctct 1426
            |||||| ||| |||||||||||
Sbjct: 511  ggtggggacataagtagctct 531
```

 Score = 56.0 bits (28), Expect = 4e-04
 Identities = 58/68 (85%)
 Strand = Plus / Plus

```
Query: 1887 agaaaggagaactatccaaaactaatttcctctgacatgtaagacgaatgatttaggtac 1946
            |||||| ||| ||||||||||||||| || ||||||||||||||| |||||| ||| |||
Sbjct: 977  agaaagtagatctatccaaaactaatatctgctgacatgtaagatgaatgacttatatac 1036
```

```
Query: 1947 gtcaaagc 1954
            ||||||||
```

Sbjct: 1037 ctcaaagc 1044

Score = 48.1 bits (24), Expect = 0.10
Identities = 37/40 (92%), Gaps = 1/40 (2%)
Strand = Plus / Plus

Query: 2188 ctccttggtatttctgggtctttctgacatcagcagagaa 2227
             ||||||||||||||||| || |||||||||||||||||||||
Sbjct: 1305 ctccttggtatttctga-tccttctgacatcagcagagaa 1343

Score = 48.1 bits (24), Expect = 0.10
Identities = 51/60 (85%)
Strand = Plus / Plus

Query: 1531 ggtgacccgaattataaaggccagcgccagaacccagatttcctaactctggtgctcttt 1590
             ||||||| |||| ||||||| | | || |||||||||||||||| ||| |||||||||
Sbjct: 624 ggtgacctgaatgataaaggtctgagctagaacccagatttcctgtctcgggtgctcttt 683

Score = 42.1 bits (21), Expect = 6.4
Identities = 27/29 (93%)
Strand = Plus / Plus

Query: 1670 tgtccaataacaggtcaacttcagagact 1698
             |||||||| |||||||||||||||||||
Sbjct: 765 tgtccaatgtcaggtcaacttcagagact 793

☐ >gi|755096|dbj|D49843.1|RABCD80C   Oryctolagus cuniculus mRNA for CD80, complete c
         Length = 950

Score = 101 bits (51), Expect = 8e-18
Identities = 150/183 (81%)
Strand = Plus / Plus

Query: 837 aaggataatttgctcaacctctggaggttttccagagcctcacctctcctggttggaaaa 896
             |||||||| ||||| |||||||||||||||||||||||||| |||| ||||| ||||| |
Sbjct: 492 aaggataagatgctccgcctctggaggttttccagagcctcgcctcgcctggatggaaga 551

Query: 897 tggagaagaattaaatgccatcaacacaacagtttcccaagatcctgaaactgagctcta 956
             |||||||||| |||| ||| ||||||| || ||| ||| ||| || || |||||||||
Sbjct: 552 tggagaagaactaaacgccgtcaacacgacggttgaccaggatttggacacggagctcta 611

Query: 957 tgctgttagcagcaaactggatttcaatatgacaaccaaccacagcttcatgtgtctcat 1016
             || ||||| |||||||||||||| |||||| ||||||||| |||||||| || ||||||||
Sbjct: 612 cagcgtcagcagtgaactggatttcaatgtgacaaataaccacagcatcgtgtgtctcat 671

```
Query: 1017 caa 1019
             |||
Sbjct: 672  caa 674
```

```
 Score = 50.1 bits (25), Expect = 0.026
 Identities = 61/73 (83%)
 Strand = Plus / Plus
```

```
Query: 613 tggcccgagtacaagaaccggaccatctttgatatcactaataacctctccattgtgatc 672
            |||||  ||||||||||||||| ||| ||    || |||| ||| |||||||||| || ||||||
Sbjct: 268 tggcctgagtacaagaaccgcaccttccccgacatcattaacaacctctcccttatgatc 327
```

```
Query: 673 ctggctctgcgcc 685
            |||||  |||||||
Sbjct: 328 ctggcactgcgcc 340
```

□ >gi|507872|gb|U10925.1|RNU10925 **L U G** Rattus norvegicus NEDH B7-1 (B7-1) mRNA, ɪ
         Length = 1152

```
 Score = 95.6 bits (48), Expect = 5e-16
 Identities = 81/92 (88%)
 Strand = Plus / Plus
```

```
Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921
            |||||  |||  ||||||  ||||||  ||||||||||||||||||  ||||||||||| ||||||
Sbjct: 795 ggtttcccaaagcctcgcctctcttggttggaaaatggaagagaattaaatggcatcaat 854
```

```
Query: 922 acaacagtttcccaagatcctgaaactgagct 953
            |||||| |||||||| |||||||||| |||||||
Sbjct: 855 acaacaatttcccaggatcctgaatctgagct 886
```

```
 Score = 46.1 bits (23), Expect = 0.41
 Identities = 23/23 (100%)
 Strand = Plus / Plus
```

```
Query: 613 tggcccgagtacaagaaccggac 635
            |||||||||||||||||||||||
Sbjct: 546 tggcccgagtacaagaaccggac 568
```

□ >gi|453381|gb|U05593.1|RRU05593 **L U G** Rattus norvegicus B7-1 mRNA, complete cds
         Length = 1030

```
 Score = 95.6 bits (48), Expect = 5e-16
 Identities = 81/92 (88%)
 Strand = Plus / Plus
```

```
Query: 862  ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921
             |||||  |||  ||||||| |||||||  ||||||||||||||||  |||||||||||  |||||||
Sbjct: 532  ggtttcccaaagcctcgcctctcttggttggaaaatggaagagaattaaatggcatcaat 591


Query: 922  acaacagtttcccaagatcctgaaactgagct 953
             ||||||| ||||||||| |||||||||| |||||||
Sbjct: 592  acaacaatttcccaggatcctgaatctgagct 623
```

☐ >gi|29789033|ref|NM_012926.1| **L U** Rattus norvegicus CD80 antigen (Cd80), mRNA
           Length = 1000

 Score = 87.7 bits (44), Expect = 1e-13
 Identities = 80/92 (86%)
 Strand = Plus / Plus

```
Query: 862  ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921
             |||||  |||  |||||| ||||||| ||||||||||||||||||  |||||||||| |||  ||
Sbjct: 521  ggtttcccaaagcctcgcctctcttggttggaaaatggaagagaattaaatggcattaat 580


Query: 922  acaacagtttcccaagatcctgaaactgagct 953
             ||||||| ||||||||| |||||||||| |||||||
Sbjct: 581  acaacaatttcccaggatcctgaatctgagct 612
```

 Score = 46.1 bits (23), Expect = 0.41
 Identities = 23/23 (100%)
 Strand = Plus / Plus

```
Query: 613  tggcccgagtacaagaaccggac 635
             |||||||||||||||||||||||
Sbjct: 272  tggcccgagtacaagaaccggac 294
```

☐ >gi|2317781|gb|AF010465.1|AF010465 **L U G** Rattus norvegicus B7.1 (B7.1) mRNA, com
           Length = 1000

 Score = 87.7 bits (44), Expect = 1e-13
 Identities = 80/92 (86%)
 Strand = Plus / Plus

```
Query: 862  ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921
             |||||  |||  |||||| |||||| ||||||||||||||||||  |||||||||| |||  ||
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Query: 922  acaacagtttcccaagatcctgaaactgagct 953
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Sbjct: 581  acaacaatttcccaggatcctgaatctgagct 612
```

```
Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus


Query: 613 tggcccgagtacaagaaccggac 635
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Sbjct: 272 tggcccgagtacaagaaccggac 294
```

☐ >gi|2853280|gb|U88622.1|RNU88622 **L U** Rattus norvegicus CD80 mRNA, complete cds
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Score = 87.7 bits (44), Expect = 1e-13
Identities = 80/92 (86%)
Strand = Plus / Plus


Query: 862 ggttttccagagcctcacctctcctggttggaaaatggagaagaattaaatgccatcaac 921
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Sbjct: 514 ggtttcccaaagcctcggctctcttggttggaaaatggaagagaattaaatggcatcaat 573


Query: 922 acaacagtttcccaagatcctgaaactgagct 953
            ||||||  |||||||| ||||||||||  |||||||
Sbjct: 574 acaacaatttcccaggatcctgaatctgagct 605
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```
Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus


Query: 613 tggcccgagtacaagaaccggac 635
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Sbjct: 265 tggcccgagtacaagaaccggac 287
```

☐ >gi|30268719|gb|AF387763.1| Meriones unguiculatus costimulatory molecule B7.1 mF
            cds
            Length = 1014

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Score = 83.8 bits (42), Expect = 2e-12
Identities = 113/134 (84%), Gaps = 2/134 (1%)
Strand = Plus / Plus


Query: 852 aacctctggaggttttccagagcctcacctctcct-ggttggaaaatggagaagaattaa 910
            |||||||||||||||| |||||||||| |  |||| | ||||||||'| |||| ||||||||
Sbjct: 496 aacctctggaggtttcccagagcctcgc-tctctttggttggaaagtggaagagaattaa 554


Query: 911 atgccatcaacacaacagtttcccaagatcctgaaactgagctctatgctgttagcagca 970
            | ||||||| ||||| ||||||||| || |||||| |||| || ||||| || || ||||
```

```
Sbjct: 555 ggggcatcaatacaaccgtttcccaggaccctgaatctgaactgtatgccgtcagtagca 614
```

>gi|37903875|gb|AY223679.1| Meriones unguiculatus costimulatory molecule B7.1 mF
              cds
        Length = 1013

Score = 83.8 bits (42), Expect = 2e-12
Identities = 113/134 (84%), Gaps = 2/134 (1%)
Strand = Plus / Plus

```
Query: 852 aacctctggaggttttccagagcctcacctctcct-ggttggaaaatggagaagaattaa 910
           |||||||||||||||| |||||||||| | |||| | ||||||||| |||| ||||||||
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            | |||||| ||||| ||||||||| || |||||| |||| || ||||| || || ||||
Sbjct: 554 ggggcatcaatacaaccgtttcccaggaccctgaatctgaactgtatgccgtcagtagca 613


Query: 971 aactggatttcaat 984
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Sbjct: 614 aactggatttcaat 627
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>gi|10566942|dbj|AB033127.1| Homo sapiens CD80 gene, promoter region, allele:ATA
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Score = 81.8 bits (41), Expect = 7e-12
Identities = 41/41 (100%)
Strand = Plus / Plus

```
Query: 1   aagtaacagaagttagaaggggaaatgtcgcctctctgaag 41
           |||||||||||||||||||||||||||||||||||||||||
Sbjct: 655 aagtaacagaagttagaaggggaaatgtcgcctctctgaag 695
```

>gi|10566941|dbj|AB033126.1| Homo sapiens CD80 gene, promoter region, allele:CTC
              Length = 690

Score = 81.8 bits (41), Expect = 7e-12
Identities = 41/41 (100%)
Strand = Plus / Plus

```
Query: 1   aagtaacagaagttagaaggggaaatgtcgcctctctgaag 41
           |||||||||||||||||||||||||||||||||||||||||
Sbjct: 650 aagtaacagaagttagaaggggaaatgtcgcctctctgaag 690
```

>gi|10566940|dbj|AB033125.1| Homo sapiens CD80 gene, promoter region, allele:CCC
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 Score = 81.8 bits (41), Expect = 7e-12
 Identities = 41/41 (100%)
 Strand = Plus / Plus

Query: 1   aagtaacagaagttagaaggggaaatgtcgcctctctgaag 41
            |||||||||||||||||||||||||||||||||||||||||
Sbjct: 650 aagtaacagaagttagaaggggaaatgtcgcctctctgaag 690

>gi|10566939|dbj|AB033124.1| Homo sapiens CD80 gene, promoter region, allele:CTC
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 Score = 81.8 bits (41), Expect = 7e-12
 Identities = 41/41 (100%)
 Strand = Plus / Plus

Query: 1   aagtaacagaagttagaaggggaaatgtcgcctctctgaag 41
            |||||||||||||||||||||||||||||||||||||||||
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>gi|47084437|gb|AC107274.11| D Rattus norvegicus 18 BAC CH230-207M17 (Children's
           Research Institute) complete sequence
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 Score = 75.8 bits (38), Expect = 5e-10
 Identities = 62/70 (88%)
 Strand = Plus / Minus

Query: 2017   ctttaaatggctttatgctagtttgacctcatttgtaaaatatttatgagaaagttctca 2076
              |||| |||||||||||||||||||||||| |||| || | |||| ||||||||||| || |||
Sbjct: 171277 ctttcaatggctttatgctagtttgatctcacttatgaaatgtttatgagaaatttgtca 171218

Query: 2077   tttaaaatga 2086
              ||||.|||||
Sbjct: 171217 tttaaaatga 171208

[Get selected sequences]   [Select all] [Deselect all]

Lambda   K   H
  1.37   0.711   1.31

Gapped
Lambda   K   H
   1.37   0.711   1.31

Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2280493
Number of Hits to DB: 35,079,557
Number of extensions: 2029161
Number of successful extensions: 17426
Number of sequences better than 10.0: 25
Number of HSP's better than 10.0 without gapping: 25
Number of HSP's gapped: 17408
Number of HSP's successfully gapped: 42
Number of extra gapped extensions for HSPs above 10.0: 17343
Length of query: 2824
Length of database: 11,051,402,435
Length adjustment: 23
Effective length of query: 2801
Effective length of database: 10,998,951,096
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Effective search space used: 30808062019896
A: 0
X1: 11 (21.8 bits)
X2: 15 (30.0 bits)
X3: 25 (50.0 bits)
S1: 12 (25.0 bits)
S2: 21 (42.1 bits)

NCBI

≋Nucleotide

| Entrez | PubMed | Nucleotide | Protein | Genome | Structure | PMC | Taxonomy | Boo |

Search | Nucleotide ▼ | for [ ] | Go | Clear |

Limits   Preview/Index   History   Clipboard   Details

| Display▾ | default ▼ | Show: | 20 ▼ | Send to | File ▼ | Get Subsequence | Feat |

☐ **1:** NM_175862. Homo sapiens CD86...[gi:29029571]   Links

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LOCUS       NM_175862              2781 bp     mRNA    linear   PRI 22-DEC-2003
DEFINITION  Homo sapiens CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)
            (CD86), transcript variant 1, mRNA.
ACCESSION   NM_175862
VERSION     NM_175862.2  GI:29029571
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2781)
  AUTHORS   Clayton,A.R., Prue,R.L., Harper,L., Drayson,M.T. and Savage,C.O.
  TITLE     Dendritic cell uptake of human apoptotic and necrotic neutrophils
            inhibits CD40, CD80, and CD86 expression and reduces allogeneic T
            cell responses: relevance to systemic vasculitis
  JOURNAL   Arthritis Rheum. 48 (8), 2362-2374 (2003)
   PUBMED   12905492
  REMARK    GeneRIF: Immature dendritic cells engulfed apoptotic and necrotic
            neutrophils, resulting in up-regulation of CD83 and class II major
            histocompatibility complex molecules, but down-regulation of CD40,
            CD80, and CD86
REFERENCE   2  (bases 1 to 2781)
  AUTHORS   Rogers,N.J., Jackson,I.M., Jordan,W.J., Hawadle,M.A., Dorling,A.
            and Lechler,R.I.
  TITLE     Cross-species costimulation: relative contributions of CD80, CD86,
            and CD40
  JOURNAL   Transplantation 75 (12), 2068-2076 (2003)
   PUBMED   12829914
  REMARK    GeneRIF: expression profiles and relative contribution in the
            porcine-human xenogeneic response
REFERENCE   3  (bases 1 to 2781)
  AUTHORS   Goto,E., Ishido,S., Sato,Y., Ohgimoto,S., Ohgimoto,K.,
            Nagano-Fujii,M. and Hotta,H.
  TITLE     c-MIR, a human E3 ubiquitin ligase, is a functional homolog of
            herpesvirus proteins MIR1 and MIR2 and has similar activity
  JOURNAL   J. Biol. Chem. 278 (17), 14657-14668 (2003)
   PUBMED   12582153
  REMARK    GeneRIF: c-MIR induced specific down-regulation of B7-2 surface
            expression through ubiquitination, rapid endocytosis, and lysosomal
            degradation
REFERENCE   4  (bases 1 to 2781)
  AUTHORS   Zhang,X., Schwartz,J.C., Almo,S.C. and Nathenson,S.G.
  TITLE     Crystal structure of the receptor-binding domain of human B7-2:
            insights into organization and signaling
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (5), 2586-2591 (2003)
   PUBMED   12606712
  REMARK    GeneRIF: B7-2 dimer observed in the B7-2/CTLA-4 complex displays a
            very hydrophilic dimer interface which provides a mechanism for
            preventing the formation of B7-1/B7-2 heterodimers
```

REFERENCE   5 (bases 1 to 2781)
   AUTHORS   Filion,L.G., Matusevicius,D., Graziani-Bowering,G.M., Kumar,A. and
              Freedman,M.S.
   TITLE   Monocyte-derived IL12, CD86 (B7-2) and CD40L expression in
              relapsing and progressive multiple sclerosis
   JOURNAL   Clin. Immunol. 106 (2), 127-138 (2003)
   PUBMED   12672403
   REMARK   GeneRIF: A key mechanism in the pathogenesis of MS is the increased
              expression of CD86 and CD40L and the increased production of IL12
              during disease progression.
REFERENCE   6 (bases 1 to 2781)
   AUTHORS   Verbovetski,I., Bychkov,H., Trahtemberg,U., Shapira,I.,
              Hareuveni,M., Ben-Tal,O., Kutikov,I., Gill,O. and Mevorach,D.
   TITLE   Opsonization of apoptotic cells by autologous iC3b facilitates
              clearance by immature dendritic cells, down-regulates DR and CD86,
              and up-regulates CC chemokine receptor 7
   JOURNAL   J. Exp. Med. 196 (12), 1553-1561 (2002)
   PUBMED   12486098
   REMARK   GeneRIF: Data show that interaction between iC3b-opsonized
              apoptotic cells and immature dendritic cells down-regulated the
              expression of CD86 and up-regulated expression of CC chemokine
              receptor 7.
REFERENCE   7 (bases 1 to 2781)
   AUTHORS   Ke,X.Y., Gribben,J., Wang,J. and Wang,D.B.
   TITLE   The identical effects of B7-1 and B7-2 on regulation of human IL-2
              gene transcription factors NF-kappa B and AP-1
   JOURNAL   Zhongguo Shi Yan Xue Ye Xue Za Zhi 10 (6), 512-518 (2002)
   PUBMED   12513711
   REMARK   GeneRIF: The identical effects of B7-1 and B7-2 on regulation of
              human IL-2 gene transcription factors NF-kappa B and AP-1.
REFERENCE   8 (bases 1 to 2781)
   AUTHORS   Shah,R., Banks,K., Patel,A., Dogra,S., Terrell,R., Powers,P.A.,
              Fenton,C., Dinauer,C.A., Tuttle,R.M. and Francis,G.L.
   TITLE   Intense expression of the b7-2 antigen presentation coactivator is
              an unfavorable prognostic indicator for differentiated thyroid
              carcinoma of children and adolescents
   JOURNAL   J. Clin. Endocrinol. Metab. 87 (9), 4391-4397 (2002)
   PUBMED   12213904
   REMARK   GeneRIF: Intense expression is an unfavorable prognostic indicator
              for differentiated thyroid carcinoma of children and adolescents
REFERENCE   9 (bases 1 to 2781)
   AUTHORS   Venuprasad,K., Banerjee,P.P., Chattopadhyay,S., Sharma,S., Pal,S.,
              Parab,P.B., Mitra,D. and Saha,B.
   TITLE   Human neutrophil-expressed CD28 interacts with macrophage B7 to
              induce phosphatidylinositol 3-kinase-dependent IFN-gamma secretion
              and restriction of Leishmania growth
   JOURNAL   J. Immunol. 169 (2), 920-928 (2002)
   PUBMED   12097397
   REMARK   GeneRIF: Leishmania major infection of macrophages cocultured with
              neutrophils results in a neutrophil-macrophage interaction via CD86
              leading to IFN-gamma secretion and restriction of Leishmania
              growth.
REFERENCE   10 (bases 1 to 2781)
   AUTHORS   Turpeinen,H., Laine,A.P., Nejentsev,S., Sjoroos,M., Ilonen,J.,
              Simell,O., Veijola,R., Knip,M., Akerblom,H.K. and Knip,M.
   TITLE   CD86 gene polymorphisms: no association with Type I diabetes among
              Finnish subjects
   JOURNAL   Diabetologia 45 (7), 1041-1042 (2002)
   PUBMED   12187923
   REMARK   GeneRIF: polymorphisms have no association with type I diabetes

```
                         among Finnish subjects
REFERENCE   11 (bases 1 to 2781)
  AUTHORS   Groth,C., Drager,R., Warnatz,K., Wolff-Vorbeck,G., Schmidt,S.,
            Eibel,H., Schlesier,M. and Peter,H.H.
    TITLE   Impaired up-regulation of CD70 and CD86 in naive (CD27-) B cells
            from patients with common variable immunodeficiency (CVID)
  JOURNAL   Clin. Exp. Immunol. 129 (1), 133-139 (2002)
   PUBMED   12100033
   REMARK   GeneRIF: Impaired up-regulation of CD70 and CD86 in naive B cells
            from patients with CVID suggests an intrinsic signalling or
            expression defect at the level of naive B cells in type I CVID.
REFERENCE   12 (bases 1 to 2781)
  AUTHORS   Zhang,X., Schwartz,J.C., Almo,S.C. and Nathenson,S.G.
    TITLE   Expression, refolding, purification, molecular characterization,
            crystallization, and preliminary X-ray analysis of the receptor
            binding domain of human B7-2
  JOURNAL   Protein Expr. Purif. 25 (1), 105-113 (2002)
   PUBMED   12071705
   REMARK   GeneRIF: expression, refolding, purification, characterization, and
            crystallization of the receptor-binding domain of human B7-2 is
            described; glycosylation is not important for proper folding of the
            receptor-binding domain of B7-2 nor for its binding to CTLA-4
REFERENCE   13 (bases 1 to 2781)
  AUTHORS   Hock,B.D., Patton,W.N., Budhia,S., Mannari,D., Roberts,P. and
            McKenzie,J.L.
    TITLE   Human plasma contains a soluble form of CD86 which is present at
            elevated levels in some leukaemia patients
  JOURNAL   Leukemia 16 (5), 865-873 (2002)
   PUBMED   11986949
   REMARK   GeneRIF: a soluble form of CD86 encoded by an alternatively spliced
            transcript is present at elevated levels in blood in some leukaemia
            patients
REFERENCE   14 (bases 1 to 2781)
  AUTHORS   Suvas,S., Singh,V., Sahdev,S., Vohra,H. and Agrewala,J.N.
    TITLE   Distinct role of CD80 and CD86 in the regulation of the activation
            of B cell and B cell lymphoma
  JOURNAL   J. Biol. Chem. 277 (10), 7766-7775 (2002)
   PUBMED   11726649
   REMARK   GeneRIF: Thus, this study is the first demonstration of a distinct
            signaling event induced by CD80 and CD86 molecules in B cell
            lymphoma.
REFERENCE   15 (bases 1 to 2781)
  AUTHORS   Vasilevko,V., Ghochikyan,A., Holterman,M.J. and Agadjanyan,M.G.
    TITLE   CD80 (B7-1) and CD86 (B7-2) are functionally equivalent in the
            initiation and maintenance of CD4+ T-cell proliferation after
            activation with suboptimal doses of PHA
  JOURNAL   DNA Cell Biol. 21 (3), 137-149 (2002)
   PUBMED   12015893
   REMARK   GeneRIF: CD80 and CD86 molecules can substitute for each other in
            the initial activation of resting CD4(+) T cells and in the
            maintenance of their proliferative response
REFERENCE   16 (bases 1 to 2781)
  AUTHORS   Re,F., Arpinati,M., Testoni,N., Ricci,P., Terragna,C., Preda,P.,
            Ruggeri,D., Senese,B., Chirumbolo,G., Martelli,V., Urbini,B.,
            Baccarani,M., Tura,S. and Rondelli,D.
    TITLE   Expression of CD86 in acute myelogenous leukemia is a marker of
            dendritic/monocytic lineage
  JOURNAL   Exp. Hematol. 30 (2), 126-134 (2002)
   PUBMED   11823047
   REMARK   GeneRIF: In AML, CD86 is a marker of monocytic/dendritic lineage
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REFERENCE   17 (bases 1 to 2781)
  AUTHORS   Niemann-Masanek,U., Mueller,A., Yard,B.A., Waldherr,R. and van der
            Woude,F.J.
  TITLE     B7-1 (CD80) and B7-2 (CD 86) expression in human tubular epithelial
            cells in vivo and in vitro
  JOURNAL   Nephron 92 (3), 542-556 (2002)
   PUBMED   12372936
  REMARK    GeneRIF: After B7-1 and B7-2 induction, proximal tubular epithelial
            cells costimulate CD28 on T lymphocytes resulting in cytokine
            production.
REFERENCE   18 (bases 1 to 2781)
  AUTHORS   Chang,T.T., Kuchroo,V.K. and Sharpe,A.H.
  TITLE     Role of the B7-CD28/CTLA-4 pathway in autoimmune disease
  JOURNAL   Curr. Dir. Autoimmun. 5, 113-130 (2002)
   PUBMED   11826754
  REMARK    GeneRIF: The B7-CD28/CTLA-4 costimulatory pathway has a dominant
            role in regulating T-cell activation. Antagonists enable graft
            survival and suppress autoimmunity.
REFERENCE   19 (bases 1 to 2781)
  AUTHORS   Schwartz,J.C., Zhang,X., Fedorov,A.A., Nathenson,S.G. and Almo,S.C.
  TITLE     Structural basis for co-stimulation by the human CTLA-4/B7-2
            complex
  JOURNAL   Nature 410 (6828), 604-608 (2001)
   PUBMED   11279501
  REMARK    GeneRIF: Structure in complex with CTLA-4; may represent a distinct
            signalling mechanism available to dimeric cell-surface receptors.
REFERENCE   20 (bases 1 to 2781)
  AUTHORS   Bugeon,L. and Dallman,M.J.
  TITLE     Costimulation of T cells
  JOURNAL   Am. J. Respir. Crit. Care Med. 162 (4 Pt 2), S164-S168 (2000)
   PUBMED   11029388
REFERENCE   21 (bases 1 to 2781)
  AUTHORS   Jeannin,P., Magistrelli,G., Aubry,J.P., Caron,G., Gauchat,J.F.,
            Renno,T., Herbault,N., Goetsch,L., Blaecke,A., Dietrich,P.Y.,
            Bonnefoy,J.Y. and Delneste,Y.
  TITLE     Soluble CD86 is a costimulatory molecule for human T lymphocytes
  JOURNAL   Immunity 13 (3), 303-312 (2000)
   PUBMED   11021528
REFERENCE   22 (bases 1 to 2781)
  AUTHORS   Reeves,R.H., Patch,D., Sharpe,A.H., Borriello,F., Freeman,G.J.,
            Edelhoff,S. and Disteche,C.
  TITLE     The costimulatory genes Cd80 and Cd86 are linked on mouse
            chromosome 16 and human chromosome 3
  JOURNAL   Mamm. Genome 8 (8), 581-582 (1997)
   PUBMED   9250865
REFERENCE   23 (bases 1 to 2781)
  AUTHORS   Jellis,C.L., Wang,S.S., Rennert,P., Borriello,F., Sharpe,A.H.,
            Green,N.R. and Gray,G.S.
  TITLE     Genomic organization of the gene coding for the costimulatory human
            B-lymphocyte antigen B7-2 (CD86)
  JOURNAL   Immunogenetics 42 (2), 85-89 (1995)
   PUBMED   7541777
REFERENCE   24 (bases 1 to 2781)
  AUTHORS   Chen,C., Gault,A., Shen,L. and Nabavi,N.
  TITLE     Molecular cloning and expression of early T cell costimulatory
            molecule-1 and its characterization as B7-2 molecule
  JOURNAL   J. Immunol. 152 (10), 4929-4936 (1994)
   PUBMED   7513726
REFERENCE   25 (bases 1 to 2781)
  AUTHORS   Freeman,G.J., Gribben,J.G., Boussiotis,V.A., Ng,J.W., Restivo,V.A.
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                    Jr., Lombard,L.A., Gray,G.S. and Nadler,L.M.
    TITLE           Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human
                    T cell proliferation
    JOURNAL         Science 262 (5135), 909-911 (1993)
    PUBMED          7694363
REFERENCE           26 (bases 1 to 2781)
    AUTHORS         Azuma,M., Ito,D., Yagita,H., Okumura,K., Phillips,J.H., Lanier,L.L.
                    and Somoza,C.
    TITLE           B70 antigen is a second ligand for CTLA-4 and CD28
    JOURNAL         Nature 366 (6450), 76-79 (1993)
    PUBMED          7694153
COMMENT             REVIEWED REFSEQ: This record has been curated by NCBI staff. The
                    reference sequence was derived from BC040261.1.
                    On Mar 18, 2003 this sequence version replaced gi:28466994.

                    Summary: This gene encodes a type I membrane protein that is a
                    member of the immunoglobulin superfamily. This protein is expressed
                    by antigen-presenting cells, and it is the ligand for two proteins
                    at the cell surface of T cells, CD28 antigen and cytotoxic
                    T-lymphocyte-associated protein 4. Binding of this protein with
                    CD28 antigen is a costimulatory signal for activation of the
                    T-cell. Binding of this protein with cytotoxic
                    T-lymphocyte-associated protein 4 negatively regulates T-cell
                    activation and diminishes the immune response. Alternative splicing
                    results in two transcript variants encoding different isoforms.
                    Additional transcript variants have been described, but their
                    full-length sequences have not been determined.

                    Transcript Variant: This variant (1) encodes the longer isoform (1)
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                    COMPLETENESS: complete on the 3' end.
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                    /note="isoform 1 is encoded by transcript variant 1; CD28
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                    [evidence IEA];
                    go_component: plasma membrane [goid 0005886] [evidence NR]
                    [pmid 7513726];
                    go_function: receptor activity [goid 0004872] [evidence
                    TAS] [pmid 7694363];
                    go_process: positive regulation of cell proliferation
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Jun 8 2004 17:01:12

NCBI   results of **BLAST**

BLASTN 2.2.9 [May-01-2004]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 1089397542-7110-63957653711.BLASTQ4

Query=
          (2781 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
          2,280,493 sequences; 11,051,402,435 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

Distribution of 145 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores

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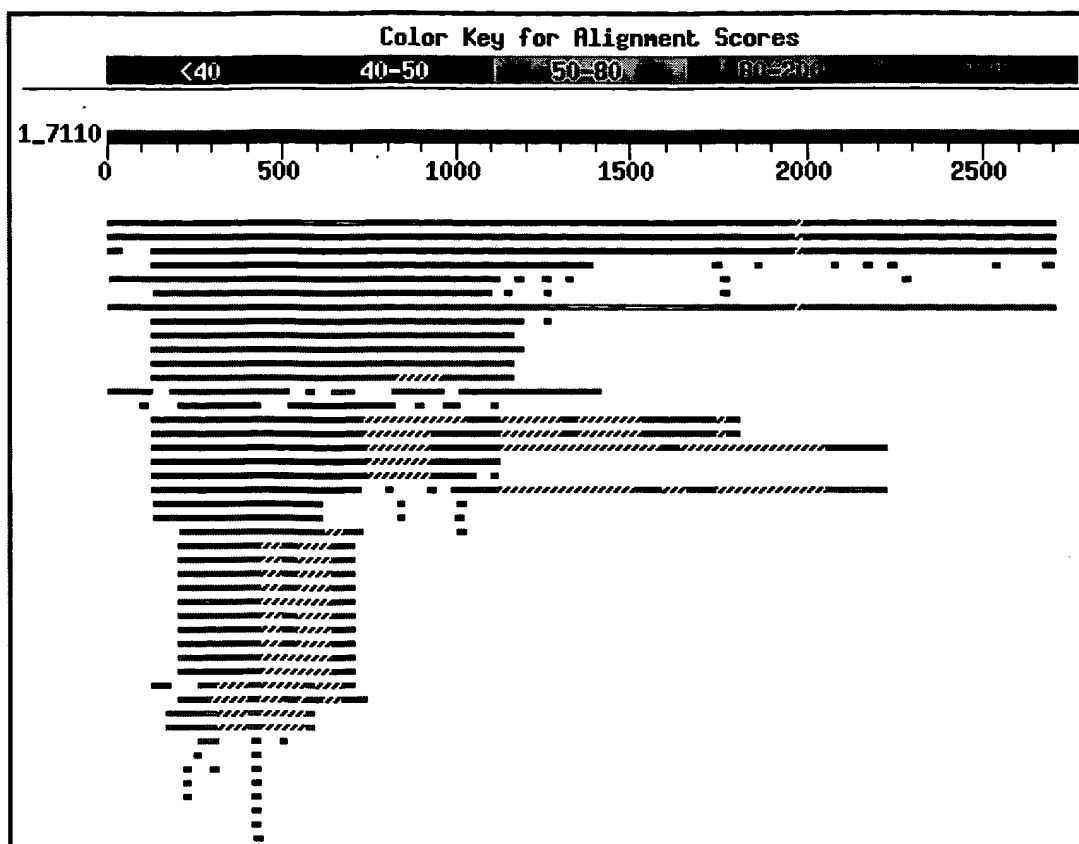
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gi|18056738|gb|AC097715.3| Homo sapiens BAC clone RP11-563A...   42   6.3
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gi|13365868|dbj|AB056772.1| Macaca fascicularis brain cDNA ...   42   6.3   G
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gi|21541280|emb|AL096864.12|HSJ993D20   Human DNA sequence fr...   42   6.3
gi|21264628|ref|NM_013437.2| Homo sapiens suppression of tu...   42   6.3   L U G

Alignments

| Get selected sequences | Select all | Deselect all |

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Strand = Plus / Plus

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Sbjct: 1081  gcgacaaaagtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttt 1140


Query: 1141  tctaccctttcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaa 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141  tctaccctttcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaa 1200


Query: 1201  gacattaccatgagtaataaggggggctccaggactccctctaagtggaatagcctccctg 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201  gacattaccatgagtaataaggggggctccaggactccctctaagtggaatagcctccctg 1260


Query: 1261  taactccagctctgctccgtatgccaagaggagactttaattctcttactgcttcttttc 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261  taactccagctctgctccgtatgccaagaggagactttaattctcttactgcttcttttc 1320


Query: 1321  acttcagagcacacttatgggccaagcccagcttaatggctcatgacctggaaataaaat 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321  acttcagagcacacttatgggccaagcccagcttaatggctcatgacctggaaataaaat 1380


Query: 1381  ttaggaccaatacctcctccagatcagattcttctcttaatttcatagattgtgnnnnnn 1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381  ttaggaccaatacctcctccagatcagattcttctcttaatttcatagattgtgtttttt 1440


Query: 1441  nnnaaatagacctctcaatttctggaaaactgccttttatctgcccagaattctaagctg 1500
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441  tttaaatagacctctcaatttctggaaaactgccttttatctgcccagaattctaagctg 1500


Query: 1501  gtgccccactgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtggga 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1501  gtgccccactgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtggga 1560


Query: 1561  cttatgtatttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgta 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1561  cttatgtatttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgta 1620


Query: 1621  atagtgtgattactatgctctagagaaaagtctacccctgctaaggagttctcatccctc 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1621  atagtgtgattactatgctctagagaaaagtctacccctgctaaggagttctcatccctc 1680


Query: 1681  tgtcagggtcagtaaggaaaacggtggcctagggtacaggcaacaatgagcagaccaacc 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1681  tgtcagggtcagtaaggaaaacggtggcctagggtacaggcaacaatgagcagaccaacc 1740


Query: 1741  taaatttggggaaattaggagaggcagagatagaacctggagccacttctatctgggctg 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1741  taaatttggggaaattaggagaggcagagatagaacctggagccacttctatctgggctg 1800
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```
Query: 1801  ttgctaatattgaggaggcttgccccacccaacaagccatagtggagagaactgaataaa 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1801  ttgctaatattgaggaggcttgccccacccaacaagccatagtggagagaactgaataaa 1860


Query: 1861  caggaaaatgccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggc 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1861  caggaaaatgccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggc 1920


Query: 1921  ctggggaagctgtgaaagaaccaaaagagatcacaatactc 1961
             |||||||||||||||||||||||||||||||||||||||||
Sbjct: 1921  ctggggaagctgtgaaagaaccaaaagagatcacaatactc 1961



 Score = 1415 bits (714), Expect = 0.0
 Identities = 714/714 (100%)
 Strand = Plus / Plus


Query: 1991  tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1991  tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050


Query: 2051  acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2051  acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2110


Query: 2111  ggtcagggagggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2170
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2111  ggtcagggagggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2170


Query: 2171  gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2171  gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230


Query: 2231  ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2231  ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290


Query: 2291  cccgggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2291  cccgggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350


Query: 2351  tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 2410
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2351  tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 2410


Query: 2411  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 2470
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 2411  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 2470


Query: 2471  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2530
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2471  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2530


Query: 2531  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc 2590
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2531  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc 2590


Query: 2591  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2650
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2591  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2650


Query: 2651  tagtttctaacatgtttttgtgcagcacagtttttaataaatgcttgttacattc 2704
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2651  tagtttctaacatgtttttgtgcagcacagtttttaataaatgcttgttacattc 2704
```

☐ >gi|25955518|gb|BC040261.1| 🇱🇺 Homo sapiens CD86 antigen (CD28 antigen ligand ⸺
             transcript variant 1, mRNA (cDNA clone MGC:34413
             IMAGE:5173789), complete cds
          Length = 2781

 Score = 3826 bits (1930), Expect = 0.0
 Identities = 1951/1961 (99%)
 Strand = Plus / Plus


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Query: 1    ggaaggcttgcacagggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    ggaaggcttgcacagggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60


Query: 61   acacacggatgagtggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   acacacggatgagtggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120


Query: 121  atccccagtgcactatgggactgagtaacattctctttgtgatggccttcctgctctctg 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  atccccagtgcactatgggactgagtaacattctctttgtgatggccttcctgctctctg 180


Query: 181  gtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaat 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  gtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaat 240


Query: 241  ttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaa 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  ttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaa 300


Query: 301  acttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagt 360
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301      acttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagt  360


Query: 361      atatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcaga  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361      atatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcaga  420


Query: 421      tcaaggacaagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattc  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421      tcaaggacaagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattc  480


Query: 481      gcatccaccagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatag  540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481      gcatccaccagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatag  540


Query: 541      taccaatttctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacg  600
                |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541      taccaatttctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacg  600


Query: 601      gttacccagaacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagt  660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601      gttacccagaacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagt  660


Query: 661      atgatggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatca  720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661      atgatggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatca  720


Query: 721      gcttgtctgtttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaa  780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721      gcttgtctgtttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaa  780


Query: 781      ctgacaagacgcggctttttatcttcacctttctctatagagcttgaggaccctcagcctc  840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781      ctgacaagacgcggctttttatcttcacctttctctatagagcttgaggaccctcagcctc  840


Query: 841      ccccagaccacattccttggattacagctgtacttccaacagttattatatgtgtgatgg  900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841      ccccagaccacattccttggattacagctgtacttccaacagttattatatgtgtgatgg  900


Query: 901      ttttctgtctaattctatggaaatggaagaagaagaagcggcctcgcaactcttataaat  960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901      ttttctgtctaattctatggaaatggaagaagaagaagcggcctcgcaactcttataaat  960


Query: 961      gtggaaccaacacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatcc  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 961      gtggaaccaacacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatcc  1020


Query: 1021     atatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcat  1080
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```
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct: 1021  atatacctgaaagatctgatgaaacccagcgtgtttttaaaagttcgaagacatcttcat  1080


Query: 1081  gcgacaaaagtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttt  1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1081  gcgacaaaagtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttt  1140


Query: 1141  tctaccctttcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaa  1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141  tctaccctttcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaa  1200


Query: 1201  gacattaccatgagtaataaggggggctccaggactccctctaagtggaatagcctccctg  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201  gacattaccatgagtaataaggggggctccaggactccctctaagtggaatagcctccctg  1260


Query: 1261  taactccagctctgctccgtatgccaagaggagactttaattctcttactgcttcttttc  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261  taactccagctctgctccgtatgccaagaggagactttaattctcttactgcttcttttc  1320


Query: 1321  acttcagagcacacttatgggccaagcccagcttaatggctcatgacctggaaataaaat  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321  acttcagagcacacttatgggccaagcccagcttaatggctcatgacctggaaataaaat  1380


Query: 1381  ttaggaccaatacctcctccagatcagattcttctcttaatttcatagattgtgnnnnnn  1440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381  ttaggaccaatacctcctccagatcagattcttctcttaatttcatagattgtgtttttt  1440


Query: 1441  nnnaaatagacctctcaatttctggaaaactgccttttatctgcccagaattctaagctg  1500
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441  tttaaatagacctctcaatttctggaaaactgccttttatctgcccagaattctaagctg  1500


Query: 1501  gtgccccactgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtggga  1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1501  gtgccccactgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtggga  1560


Query: 1561  cttatgtatttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgta  1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1561  cttatgtatttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgta  1620


Query: 1621  atagtgtgattactatgctctagagaaaagtctacccctgctaaggagttctcatccctc  1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1621  atagtgtgattactatgctctagagaaaagtctacccctgctaaggagttctcatccctc  1680


Query: 1681  tgtcagggtcagtaaggaaaacggtggcctagggtacaggcaacaatgagcagaccaacc  1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1681  tgtcagggtcagtaaggaaaacggtggcctagggtacaggcaacaatgagcagaccaacc  1740


Query: 1741  taaatttggggaaattaggagaggcagagatagaacctggagccacttctatctgggctg  1800
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```
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1741 taaatttggggaaattaggagaggcagagatagaacctggagccacttctatctgggctg 1800


Query: 1801 ttgctaatattgaggaggcttgccccacccaacaagccatagtggagagaactgaataaa 1860
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1801 ttgctaatattgaggaggcttgccccacccaacaagccatagtggagagaactgaataaa 1860


Query: 1861 caggaaaatgccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggc 1920
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1861 caggaaaatgccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggc 1920


Query: 1921 ctggggaagctgtgaaagaaccaaaagagatcacaatactc 1961
       |||||||||||||||||||||||||||||||||||||||||
Sbjct: 1921 ctggggaagctgtgaaagaaccaaaagagatcacaatactc 1961
```

```
Score = 1415 bits (714), Expect = 0.0
Identities = 714/714 (100%)
Strand = Plus / Plus
```

```
Query: 1991 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1991 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050


Query: 2051 acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2110
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2051 acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2110


Query: 2111 ggtcagggaggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2170
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2111 ggtcagggaggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2170


Query: 2171 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2171 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230


Query: 2231 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2231 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290


Query: 2291 cccgggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2291 cccgggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350


Query: 2351 tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 2410
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2351 tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 2410
```

```
Query: 2411  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag  2470
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2411  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag  2470


Query: 2471  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat  2530
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2471  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat  2530


Query: 2531  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc  2590
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2531  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc  2590


Query: 2591  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc  2650
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2591  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc  2650


Query: 2651  tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc  2704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2651  tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc  2704
```

☐ >gi|29029570|ref|NM_006889.2| [L U G] Homo sapiens CD86 antigen (CD28 antigen liga
         (CD86), transcript variant 2, mRNA
             Length = 2794

 Score = 3578 bits (1805), Expect = 0.0
 Identities = 1823/1832 (99%)
 Strand = Plus / Plus

```
Query: 130  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc  189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc  202


Query: 190  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact  249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact  262


Query: 250  ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc  309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263  ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc  322


Query: 310  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc  369
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc  382


Query: 370  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca  442
```

```
Query:  430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc  489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  443  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc  502


Query:  490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  503  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  562


Query:  550  ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccag  609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  563  ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccag  622


Query:  610  aacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggta  669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  623  aacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggta  682


Query:  670  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  683  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  742


Query:  730  tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga  789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  743  tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga  802


Query:  790  cgcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc  849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  803  cgcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc  862


Query:  850  acattccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtc  909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  863  acattccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtc  922


Query:  910  taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca  969
             ||||||||||||||||||·|||||||||||||||||||||||||||||||||||||||||
Sbjct:  923  taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca  982


Query:  970  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||·|||||
Sbjct:  983  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1042


Query: 1030  aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1043  aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1102


Query: 1090  gtgatacatgtttttaattaaagagtaaagcccatacaagtattcatttttttctaccctt 1149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1103  gtgatacatgtttttaattaaagagtaaagcccatacaagtattcatttttttctaccctt 1162
```

```
Query:  1150  tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc  1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1163  tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc  1222


Query:  1210  atgagtaataagggggctccaggactccctctaagtggaatagcctccctgtaactccag  1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1223  atgagtaataagggggctccaggactccctctaagtggaatagcctccctgtaactccag  1282


Query:  1270  ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag  1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1283  ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag  1342


Query:  1330  cacacttatgggccaagcccagcttaatggctcatgacctggaaataaaatttaggacca  1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1343  cacacttatgggccaagcccagcttaatggctcatgacctggaaataaaatttaggacca  1402


Query:  1390  atacctcctccagatcagattcttctcttaatttcatagattgtgnnnnnnnnnaaatag  1449
              |||||||||||||||||||||||||||||||||||||||||||||||       ||||||
Sbjct:  1403  atacctcctccagatcagattcttctcttaatttcatagattgtgtttttttttaaatag  1462


Query:  1450  acctctcaatttctggaaaactgccttttatctgcccagaattctaagctggtgccccac  1509
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1463  acctctcaatttctggaaaactgccttttatctgcccagaattctaagctggtgccccac  1522


Query:  1510  tgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtgggacttatgtat  1569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1523  tgaatcttgtgtacctgtgactaaacaactacctcctcagtctgggtgggacttatgtat  1582


Query:  1570  ttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgtaatagtgtga  1629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1583  ttatgaccttatagtgttaatatcttgaaacatagagatctatgtactgtaatagtgtga  1642


Query:  1630  ttactatgctctagagaaaagtctacccctgctaaggagttctcatccctctgtcagggt  1689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1643  ttactatgctctagagaaaagtctacccctgctaaggagttctcatccctctgtcagggt  1702


Query:  1690  cagtaaggaaaacggtggcctagggtacaggcaacaatgagcagaccaacctaaatttgg  1749
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1703  cagtaaggaaaacggtggcctagggtacaggcaacaatgagcagaccaacctaaatttgg  1762


Query:  1750  ggaaattaggagaggcagagatagaacctggagccacttctatctgggctgttgctaata  1809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1763  ggaaattaggagaggcagagatagaacctggagccacttctatctgggctgttgctaata  1822


Query:  1810  ttgaggaggcttgccccacccaacaagccatagtggagagaactgaataaacaggaaaat  1869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1823  ttgaggaggcttgccccacccaacaagccatagtggagagaactgaataaacaggaaaat  1882
```

```
Query:  1870  gccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggcctggggaag  1929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1883  gccagagcttgtgaaccctgtttctcttgaagaactgactagtgagatggcctggggaag  1942


Query:  1930  ctgtgaaagaaccaaaagagatcacaatactc  1961
              ||||||||||||||||||||||||||||||||
Sbjct:  1943  ctgtgaaagaaccaaaagagatcacaatactc  1974
```

 Score = 1415 bits (714), Expect = 0.0
 Identities = 714/714 (100%)
 Strand = Plus / Plus

```
Query:  1991  tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa  2050
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2004  tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa  2063


Query:  2051  acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt  2110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2064  acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt  2123


Query:  2111  ggtcagggaggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga  2170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2124  ggtcagggaggggttttggtgatacccaagttattgggatgtcatcttcctggaagcaga  2183


Query:  2171  gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt  2230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2184  gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt  2243


Query:  2231  ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca  2290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2244  ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca  2303


Query:  2291  cccgggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc  2350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2304  cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc  2363


Query:  2351  tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca  2410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2364  tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca  2423


Query:  2411  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag  2470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2424  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag  2483


Query:  2471  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat  2530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  2484  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat  2543
```

```
Query: 2531  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc  2590
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2544  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc  2603


Query: 2591  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc  2650
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2604  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc  2663


Query: 2651  tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc  2704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2664  tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc  2717
```

☐ >gi|439838|gb|U04343.1|HSU04343 **L U G** Human CD86 antigen mRNA, complete cds
             Length = 1424

Score = 2504 bits (1263), Expect = 0.0
Identities = 1263/1263 (100%)
Strand = Plus / Plus

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Query: 130  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc  189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 143  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc  202


Query: 190  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact  249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 203  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact  262


Query: 250  ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc  309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 263  ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc  322


Query: 310  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc  369
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 323  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc  382


Query: 370  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 383  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca  442


Query: 430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc  489
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 443  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc  502


Query: 490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  549
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 503  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  562
```

```
Query:  550  ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccag  609
             ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct:  563  ctaatataacagaaatgtgtacataaatttgacctgctcatctatacacggttacccag   622


Query:  610  aacctaagaagatgagtgtgttttgctaagaaccaagaattcaactatcgagtatgatggta  669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  623  aacctaagaagatgagtgtgttttgctaagaaccaagaattcaactatcgagtatgatggta  682


Query:  670  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  683  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  742


Query:  730  tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga  789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  743  tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga  802


Query:  790  cgcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc  849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  803  cgcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc  862


Query:  850  acattccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtc  909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  863  acattccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtc  922


Query:  910  taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca  969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  923  taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca  982


Query:  970  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg  1029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  983  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg  1042


Query:  1030  aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa  1089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1043  aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa  1102


Query:  1090  gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt  1149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1103  gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt  1162


Query:  1150  tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc  1209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1163  tcctttgtaagttcctgggcaacctttttgatttcttccagaaggcaaaaagacattacc  1222


Query:  1210  atgagtaataaggggggctccaggactccctctaagtggaatagcctccctgtaactccag  1269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1223  atgagtaataaggggggctccaggactccctctaagtggaatagcctccctgtaactccag  1282
```

```
Query: 1270  ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag  1329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1283  ctctgctccgtatgccaagaggagactttaattctcttactgcttcttttcacttcagag  1342


Query: 1330  cacacttatgggccaagcccagcttaatggctcatgacctggaaataaaatttaggacca  1389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1343  cacacttatgggccaagcccagcttaatggctcatgacctggaaataaaatttaggacca  1402


Query: 1390  ata  1392
              |||
Sbjct: 1403  ata  1405
```

☐ >gi|416368|gb|L25259.1|HUMB72A **L U G** Human CTLA4 counter-receptor (B7-2) mRNA, ⟨
          Length = 1112

Score = 2204 bits (1112), Expect = 0.0
Identities = 1112/1112 (100%)
Strand = Plus / Plus

```
Query: 11   cacagggtgaaagctttgcttctctgctgctgtaacagggactagcacagacacacggat  70
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    cacagggtgaaagctttgcttctctgctgctgtaacagggactagcacagacacacggat  60


Query: 71   gagtggggtcatttccagatattaggtcacagcagaagcagccaaaatggatccccagtg  130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   gagtggggtcatttccagatattaggtcacagcagaagcagccaaaatggatccccagtg  120


Query: 131  cactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctcc  190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  cactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctcc  180


Query: 191  tctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaactc  250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  tctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaactc  240


Query: 251  tcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttct  310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  tcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttct  300


Query: 311  gaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccg  370
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  gaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccg  360


Query: 371  cacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaa  430
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  cacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaa  420


Query: 431  gggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacca  490
```

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                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  421   gggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacca   480


Query:  491   gatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttc   550
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  481   gatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttc   540


Query:  551   taatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccaga   610
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  541   taatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccaga   600


Query:  611   acctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggtat   670
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  601   acctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggtat   660


Query:  671   tatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgt   730
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  661   tatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgt   720


Query:  731   ttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagac   790
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  721   ttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagac   780


Query:  791   gcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacca   850
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  781   gcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacca   840


Query:  851   cattccttggattacagctgtacttccaacagttattatatgtgtgatggtttttctgtct   910
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  841   cattccttggattacagctgtacttccaacagttattatatgtgtgatggtttttctgtct   900


Query:  911   aattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaa   970
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  901   aattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaa   960


Query:  971   cacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctga   1030
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  961   cacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctga   1020


Query:  1031  aagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaag   1090
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  1021  aagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaag   1080


Query:  1091  tgatacatgttttttaattaaagagtaaagccc   1122
                    |||||||||||||||||||||||||||||||||||
Sbjct:  1081  tgatacatgttttttaattaaagagtaaagccc   1112
```

☐ >gi|49456642|emb|CR541844.1| Homo sapiens full open reading frame cDNA clone RZI
            gene CD86, CD86 antigen (CD28 antigen ligand 2, B7-2
            antigen); complete cds, without stopcodon
          Length = 969

 Score = 1921 bits (969), Expect = 0.0
 Identities = 969/969 (100%)
 Strand = Plus / Plus

Query: 135   atgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctcctctg 194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1   atgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctcctctg 60

Query: 195   aagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaa 254
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   aagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaa 120

Query: 255   aaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaat 314
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121   aaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaat 180

Query: 315   gaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcaca 374
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181   gaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcaca 240

Query: 375   agttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggc 434
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241   agttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggc 300

Query: 435   ttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccaccagatg 494
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301   ttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccaccagatg 360

Query: 495   aattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttctaat 554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361   aattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttctaat 420

Query: 555   ataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccagaacct 614
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421   ataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccagaacct 480

Query: 615   aagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggtattatg 674
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481   aagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggtattatg 540

Query: 675   cagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgtttca 734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541   cagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgtttca 600

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Query: 735  ttccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagacgcgg 794
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  ttccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaagacgcgg 660


Query: 795  cttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagaccacatt 854
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  cttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagaccacatt 720


Query: 855  ccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtctaatt 914
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  ccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtctaatt 780


Query: 915  ctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaacaca 974
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  ctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaaccaacaca 840


Query: 975  atggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctgaaaga 1034
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  atggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctgaaaga 900


Query: 1035 tctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaagtgat 1094
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  tctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaagtgat 960


Query: 1095 acatgtttt 1103
            |||||||||
Sbjct: 961  acatgtttt 969
```

☐ >gi|16572839|gb|AC068630.21| 🄳 Homo sapiens 3 BAC RP11-289N10 (Roswell Park Canc
           Library) complete sequence
         Length = 164161

 Score = 1798 bits (907), Expect = 0.0
 Identities = 944/957 (98%), Gaps = 3/957 (0%)
 Strand = Plus / Minus

```
Query: 1008  agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 1067
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86502 agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 86443


Query: 1068  aagacatcttcatgcgacaaaagtgatacatgtttttaattaaagagtaaagcccataca 1127
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86442 aagacatcttcatgcgacaaaagtgatacatgtttttaattaaagagtaaagcccataca 86383


Query: 1128  agtattcattttttctaccctttcctttgtaagttcctgggcaacctttttgatttcttc 1187
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86382 agtattcattttttctaccctttcctttgtaagttcctgggcaacctttttgatttcttc 86323
```

```
Query: 1188  cagaaggcaaaaagacattaccatgagtaataaggggggctccaggactccctctaagtgg 1247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86322 cagaaggcaaaaagacattaccatgagtaataaggggggctccaggactccctctaagtgg 86263


Query: 1248  aatagcctccctgtaactccagctctgctccgtatgccaagaggagactttaattctctt 1307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86262 aatagcctccctgtaactccagctctgctccgtatgccaagaggagactttaattctctt 86203


Query: 1308  actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 1367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86202 actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 86143


Query: 1368  ctggaaataaaatttaggaccaatacctcctccagatcagattcttctcttaatttcata 1427
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86142 ctggaaataaaatttaggaccaatacctcctccagatcagattcttctcttaatttcata 86083


Query: 1428  gattgtgnnnnnnnnnn-aaatagacctctcaatttctggaaaactgccttttatctgccc 1486
              |||||||          ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 86082 gattgtgtttttttttttaaatagacctctcaatttctggaaaactgccttttatctgccc 86023


Query: 1487  agaattctaagctggtgccccactgaatcttgtgt--acctgtgactaaacaactacctc 1544
              ||||||||||||||||||||||||||||||| |||||   ||||||||||||||||||||
Sbjct: 86022 agaattctaagctggtgccccactgaattttgtgtgtacctgtgactaaacaactacctc 85963


Query: 1545  ctcagtctgggtgggacttatgtatttatgaccttatagtgttaatatcttgaaacatag 1604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85962 ctcagtctgggtgggacttatgtatttatgaccttatagtgttaatatcttgaaacatag 85903


Query: 1605  agatctatgtactgtaatagtgtgattactatgctctagagaaaagtctacccctgctaa 1664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85902 agatctatgtactgtaatagtgtgattactatgctctagagaaaagtctacccctgctaa 85843


Query: 1665  ggagttctcatccctctgtcagggtcagtaaggaaaacggtggcctagggtacaggcaac 1724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85842 ggagttctcatccctctgtcagggtcagtaaggaaaacggtggcctagggtacaggcaac 85783


Query: 1725  aatgagcagaccaacctaaatttggggaaattaggagaggcagagatagaacctggagcc 1784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85782 aatgagcagaccaacctaaatttggggaaattaggagaggcagagatagaacctggagcc 85723


Query: 1785  acttctatctgggctgttgctaatattgaggaggcttgccccacccaacaagccatagtg 1844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85722 acttctatctgggctgttgctaatattgaggaggcttgccccacccaacaagccatagtg 85663


Query: 1845  gagagaactgaataaacaggaaaatgccagagcttgtgaaccctgtttctcttgaagaac 1904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85662 gagagaactgaataaacaggaaaatgccagagcttgtgaaccctgtttctcttgaagaac 85603
```

```
Query: 1905  tgactagtgagatggcctggggaagctgtgaaagaaccaaaagagatcacaatactc 1961
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85602 tgactagtgagatggcctggggaagctgtgaaagaaccaaaagagatcacaatactc 85546
```

```
 Score = 1415 bits (714), Expect = 0.0
 Identities = 714/714 (100%)
 Strand = Plus / Minus
```

```
Query: 1991  tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 2050
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85516 tcttgatccacagaaatacatgaaatgtctggtctgtccaccccatcaacaagtcttgaa 85457
```

```
Query: 2051  acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 2110
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85456 acaagcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggt 85397
```

```
Query: 2111  ggtcagggagggtttggtgatacccaagttattgggatgtcatcttcctggaagcaga 2170
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85396 ggtcagggagggtttggtgatacccaagttattgggatgtcatcttcctggaagcaga 85337
```

```
Query: 2171  gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 2230
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85336 gctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggacttt 85277
```

```
Query: 2231  ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 2290
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85276 ccactcctggctgagagaggaagagctgcaacggaattaggaagaccaagacacagatca 85217
```

```
Query: 2291  cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 2350
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85216 cccggggcttacttagcctacagatgtcctacgggaacgtgggctggcccagcatagggc 85157
```

```
Query: 2351  tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 2410
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85156 tagcaaatttgagttggatgattgtttttgctcaaggcaaccagaggaaacttgcataca 85097
```

```
Query: 2411  gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 2470
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85096 gagacagatatactgggagaaatgactttgaaaacctggctctaaggtgggatcactaag 85037
```

```
Query: 2471  ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 2530
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 85036 ggatggggcagtctctgcccaaacataaagagaactctggggagcctgagccacaaaaat 84977
```

```
Query: 2531  gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc 2590
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84976 gttcctttattttatgtaaaccctcaagggttatagactgccatgctagacaagcttgtc 84917
```

```
Query: 2591   catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 2650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84916  catgtaatattcccatgtttttaccctgcccctgccttgattagactcctagcacctggc 84857


Query: 2651   tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc 2704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 84856  tagtttctaacatgttttgtgcagcacagtttttaataaatgcttgttacattc 84803
```


 Score = 668 bits (337), Expect = 0.0
 Identities = 337/337 (100%)
 Strand = Plus / Minus


```
Query: 180      ggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaa 239
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 102427  ggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaa 102368


Query: 240      tttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaa 299
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 102367  tttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaa 102308


Query: 300      aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 359
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||.||
Sbjct: 102307  aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 102248


Query: 360      tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 419
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 102247  tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 102188


Query: 420      atcaaggacaagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgatt 479
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 102187  atcaaggacaagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgatt 102128


Query: 480      cgcatccaccagatgaattctgaactgtcagtgcttg 516
                |||||||||||||||||||||||||||||||||||||
Sbjct: 102127  cgcatccaccagatgaattctgaactgtcagtgcttg 102091
```


 Score = 595 bits (300), Expect = e-166
 Identities = 303/304 (99%)
 Strand = Plus / Minus


```
Query: 516     gctaacttcagtcaacctgaaatagtaccaatttctaatataacagaaaatgtgtacata 575
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 99741   gctaacttcagtcaacctgaaatagtaccaatttctaatataacagaaaatgtgtacata 99682


Query: 576     aatttgacctgctcatctatacacggttacccagaacctaagaagatgagtgttttgcta 635
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 99681 aatttgacctgctcatctatacacggttacccagaacctaagaagatgagtgttttgcta 99622


Query: 636    agaaccaagaattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtc 695
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct: 99621 agaaccaagaattcaactatcgagtatgatggtgttatgcagaaatctcaagataatgtc 99562


Query: 696    acagaactgtacgacgtttccatcagcttgtctgtttcattccctgatgttacgagcaat 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 99561 acagaactgtacgacgtttccatcagcttgtctgtttcattccctgatgttacgagcaat 99502


Query: 756    atgaccatcttctgtattctggaaactgacaagacgcggcttttatcttcacctttctct 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 99501 atgaccatcttctgtattctggaaactgacaagacgcggcttttatcttcacctttctct 99442


Query: 816    atag 819
              ||||
Sbjct: 99441 atag 99438
```

```
 Score =  293 bits (148), Expect = 1e-75
 Identities = 148/148 (100%)
 Strand = Plus / Minus
```

```
Query: 817    tagagcttgaggaccctcagcctcccccagaccacattccttggattacagctgtacttc 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 96676 tagagcttgaggaccctcagcctcccccagaccacattccttggattacagctgtacttc 96617


Query: 877    caacagttattatatgtgtgatggttttctgtctaattctatggaaatggaagaagaaga 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 96616 caacagttattatatgtgtgatggttttctgtctaattctatggaaatggaagaagaaga 96557


Query: 937    agcggcctcgcaactcttataaatgtgg 964
              ||||||||||||||||||||||||||||
Sbjct: 96556 agcggcctcgcaactcttataaatgtgg 96529
```

```
 Score =  258 bits (130), Expect = 6e-65
 Identities = 130/130 (100%)
 Strand = Plus / Minus
```

```
Query: 1       ggaaggcttgcacagggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 150564 ggaaggcttgcacagggtgaaagctttgcttctctgctgctgtaacagggactagcacag 150505


Query: 61      acacacggatgagtggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 150504 acacacggatgagtggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 150445
```

```
Query: 121    atccccagtg 130
              ||||||||||
Sbjct: 150444 atccccagtg 150435
```

```
 Score =  105 bits (53), Expect = 5e-19
 Identities = 53/53 (100%)
 Strand = Plus / Minus
```

```
Query: 130    gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 182
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 114338 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 114286
```

```
 Score = 93.7 bits (47), Expect = 2e-15
 Identities = 47/47 (100%)
 Strand = Plus / Minus
```

```
Query: 963   ggaaccaacacaatggagagggaagagagtgaacagaccaagaaaag 1009
             |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 87891 ggaaccaacacaatggagagggaagagagtgaacagaccaagaaaag 87845
```

```
□ >gi|13650019|gb|AF344861.1|AF344861    Cercopithecus aethiops CD86 protein mRNA, co
          Length = 1062

 Score = 1796 bits (906), Expect = 0.0
 Identities = 1023/1062 (96%)
 Strand = Plus / Plus
```

```
Query: 130   gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1     gcactatgggactgattaacattctctttgtgatggccttcctgctctctggtgctgctc 60
```

```
Query: 190   ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249
             | |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct: 61    ccctgaagattcaagcttatttcaatgagactgcagacctgccatgccagtttgcaaact 120
```

```
Query: 250   ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309
             |||||||| |||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct: 121   ctcaaaaccgaagcctgagtgagctagtagtattttggcagaaccaggaaaacttggttc 180
```

```
Query: 310   tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369
             |||||||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||
Sbjct: 181   tgaatgaggtatacttaggccaagagaaatttgacagcgttcattccaagtatatgggcc 240
```

```
Query: 370   gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429
             |||||||||||||| |||| |||||||||||||||||||||| |||||||||||||||||
Sbjct: 241   gcacaagttttgatccggagagttggaccctgagacttcacaaccttcagatcaaggaca 300
```

```
Query:  430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc  489
             ||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||||
Sbjct:  301  agggcttgtatcaatgtatcatccatcacaaaaggcccacaggaatgatccgcatccacc  360


Query:  490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  549
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct:  361  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtcccaattt  420


Query:  550  ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccag  609
             ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct:  421  ctaatataacagaaaatatgtacataaatttgacctgctcatctatacacggttacccag  480


Query:  610  aacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggta  669
             |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  481  aacctgagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggtg  540


Query:  670  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  541  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  600


Query:  730  tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga  789
             ||||||||||||||||||||||||| ||||||||||||||||| |||||||||||||||||
Sbjct:  601  tttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaaga  660


Query:  790  cgcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc  849
             | |  ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  661  cacagcttttatcctcacctttctctatagagcttgaggaccctcagcctcccccagacc  720


Query:  850  acattccttggattacagctgtacttccaacagttattatatgtgtgatggtttttctgtc  909
             ||||  ||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct:  721  acatcccttggattacagctgtacttccaacagttattatatgtgtgatggctttctgtc  780


Query:  910  taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca  969
             ||||||||||||||||| ||||||||||||| ||||||||||||||||||| ||||||||
Sbjct:  781  taattctatggaaatgcaagaagaagaagcagcctcgcaactcttataaacgtggaacca  840


Query:  970  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg  1029
             |||||||||||||||||||| ||||||||||| |||||||||||||||| || |||||||
Sbjct:  841  acacaatggagagggaagaaagtgaacagaccaaaaaaagagaaaaaattaatgtacctg  900


Query:  1030 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa  1089
             ||||||||||||||| |||| |||||||||||||||| ||||||| |||||||||||||||
Sbjct:  901  aaagatctgatgaaacccaatgtgtttttaaaagtttgaagacaccttcatgcgacaaaa  960


Query:  1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctacccct  1149
             ||||||| |||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct:  961  gtgatacacgtttttaattaaagagtaaagcccatacaagtattcattctttctacccct  1020
```

```
Query: 1150  tcctttgtaagttcctgggcaacctttttgatttcttccaga 1191
              |||||||||||||| |||||||||||||||||||||||||||||
Sbjct: 1021  tcctttgtaagtttctgggcaacctttttgatttcttccaga 1062
```

☐ >gi|13650011|gb|AF344857.1|AF344857   Macaca mulatta CD86 protein precursor, mRNA,
        Length = 1048

 Score = 1784 bits (900), Expect = 0.0
 Identities = 1002/1036 (96%)
 Strand = Plus / Plus

```
Query: 129  tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13   tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 72
```

```
Query: 189  cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac 248
             || ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 73   cccctgaagattcaagcttatttcaatgagactgcagacctgccatgccagtttgcaaac 132
```

```
Query: 249  tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt 308
             |||||||||| ||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct: 133  tctcaaaaccgaagcctgagtgagctagtagtattttggcagaaccaggaaaacttggtt 192
```

```
Query: 309  ctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggc 368
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 193  ctgaatgaggtatacttaggcaaagagaaatttgacagcgttcattccaagtatatgggc 252
```

```
Query: 369  cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428
             ||||||||||||| |||| ||||||||||||||| |||||||| ||||||||||||||||
Sbjct: 253  cgcacaagttttgatccggagagttggaccctgaggcttcacaaccttcagatcaaggac 312
```

```
Query: 429  aagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccac 488
             ||||||||||||||||||||||||||| ||||||| ||||||||||||||| ||||||||
Sbjct: 313  aagggcttgtatcaatgtatcatccaccacaaaaggcccacaggaatgatccgcatccac 372
```

```
Query: 489  cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt 548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 373  cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtcccaatt 432
```

```
Query: 549  tctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccca 608
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 433  tctaatataacagaaaatatgtacataaatttgacctgctcatctatacacggttaccca 492
```

```
Query: 609  gaacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggt 668
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 493  gaacctgagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggt 552
```

```
Query:  669  attatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct  728
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  553  gttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct  612


Query:  729  gtttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaag  788
             |||||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||
Sbjct:  613  gtttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaag  672


Query:  789  acgcggcttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagac  848
             || | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:  673  acacagcttttatcctcacctttctctatagagcttgaggaccctcagcctcccccagac  732


Query:  849  cacattccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgt  908
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct:  733  cacatcccttggattacagctgtacttccaacagttattatatgtgtgatggctttctgt  792


Query:  909  ctaattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacc  968
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct:  793  ctaattctatggaaatggaagaagaagaagcagcctcgcaactcttataaatgtggaacc  852


Query:  969  aacacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacct  1028
             ||||||||||||||||||||||||||||||||| ||||||||||||||| || |||||
Sbjct:  853  aacacaatggagagggaagagagtgaacagaccaaaaaaagagaaaaaattaatgtacct  912


Query:  1029 gaaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaa  1088
             |||||||||||||||||||| |||||||||||||| ||||||| ||||||||||||||||
Sbjct:  913  gaaagatctgatgaagcccaatgtgtttttaaaagtttgaagacaccttcatgcgacaaa  972


Query:  1089 agtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccct  1148
             |||||||| |||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct:  973  agtgatacacgtttttaattaaagagtaaagcccatacaagtattcattctttctaccct  1032


Query:  1149 ttcctttgtaagttcc  1164
             ||||||||||||||||
Sbjct:  1033 ttcctttgtaagttcc  1048
```

☐ >gi|13650000|gb|AF344840.1|AF344840   Cercocebus torquatus atys CD86 protein precu
                Length = 1062

 Score = 1780 bits (898), Expect = 0.0
 Identities = 1021/1062 (96%)
 Strand = Plus / Plus


```
Query:  130  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc  189
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||.|||||
Sbjct:  1    gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc  60


Query:  190  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact  249
```

```
             |  |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct:  61   ccctgaagattcaagcttatttcaatgagactgcagacctgccatgccagtttgcaaact 120


Query: 250   ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309
             ||||||||| ||||||||||||||||||||||||||||| | |||||||||||||||||
Sbjct: 121   ctcaaaaccgaagcctgagtgagctagtagtattttggcagaatcaggaaaacttggttc 180


Query: 310   tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369
             ||||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||||
Sbjct: 181   tgaatgaggtatacttaggcagagagaaatttgacagcgttcattccaagtatatgggcc 240


Query: 370   gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429
             |||||||||||| |||||||||||||||||||||| ||||||| |||||||||||||||||
Sbjct: 241   gcacaagttttgatccggacagttggaccctgaggcttcacaaccttcagatcaaggaca 300


Query: 430   agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489
             |||||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Sbjct: 301   agggcttgtatcaatgtatcatccatcacaaaaggcccacaggaatgatccgcatccacc 360


Query: 490   agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt 549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 361   agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtcccaattt 420


Query: 550   ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccag 609
             |||||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||
Sbjct: 421   ctaatataacagaaaatatgtacataaatttgacctgttcatctatacacggttacccag 480


Query: 610   aacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggta 669
             |||||  |||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct: 481   aacctgagaagatgagtgtttttgctaagaaccaagaatccaactatcgagtatgatggcg 540


Query: 670   ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg 729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541   ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg 600


Query: 730   tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga 789
             |||||||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||
Sbjct: 601   tttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaaga 660


Query: 790   cgcggctttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc 849
             | | |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661   cacagctttatcctcacctttctctatagagcttgaggaccctcagcctcccccagacc 720


Query: 850   acattccttggattacagctgtacttccaacagttattatatgtgtgatggttttctgtc 909
             |||| |||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 721   acatcccttggattacagctgtacttccaacagttattatatgtgtgatggctttctgtc 780


Query: 910   taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca 969
```

```
           ||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||||
Sbjct: 781 taattctatggaaatggaagaagaagaagcagcctcgcaactcttataactgtggaacca 840


Query: 970  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg 1029
            |||||||||||||||||||||||||||||||||||||| ||||||||||||| || |||||||
Sbjct: 841  acacaatggagagggaagagagtgaacagaccaaaaaaagagaaaaaattaatgtacctg 900


Query: 1030 aaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaaa 1089
            |||||||||||||||||||| ||||||||||||| ||||||| ||||||||||||||||||
Sbjct: 901  aaagatctgatgaagcccaatgtgtttttaaaagtttgaagacaccttcatgcgacaaaa 960


Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcattttttctaccctt 1149
            |||||||   |||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct: 961  gtgatacgcatttttaattaaagagtaaagcccatacaagtattcattctttctaccctt 1020


Query: 1150 tcctttgtaagttcctgggcaacctttttgatttcttccaga 1191
            ||||||||||||| |||||||||||||||||||||||||||||
Sbjct: 1021 tcctttgtaagtttctgggcaacctttttgatttcttccaga 1062




□ >gi|13655490|gb|AF344851.1|AF344851    Macaca nemestrina CD86 protein precursor, mF
            Length = 1044

 Score = 1721 bits (868), Expect = 0.0
 Identities = 994/1036 (95%)
 Strand = Plus / Plus


Query: 130  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 60


Query: 190  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249
            | |||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||
Sbjct: 61   ccctgaagattcaagcttacttcaatgagactgcagacctgccatgccagtttgcaaact 120


Query: 250  ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309
            |||||||| ||||||||||||||||||||||||||||||||| |||||||||||||||||
Sbjct: 121  ctcaaaaccgaagcctgagtgagctagtagtattttggcagaaccaggaaaacttggttc 180


Query: 310  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct: 181  tgaatgaggtatacttaggcaaagagaaatttgacagcgttcattccaagtatatgggcc 240


Query: 370  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429
            ||||||| ||||||| |||| |||||||||||||| |||| ||| |||||||||||||||
Sbjct: 241  gcacaagatttgatccggagagttggaccctgaggcttcgcaaccttcagatcaaggaca 300


Query: 430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489
            ||||||||||||||||||||||||||||| |||||||| |||||||||||||| |||||||
```

```
Sbjct: 301  agggcttgtatcaatgtatcatccaccacaaaaggcccacaggaatgatccgcatccacc  360


Query: 490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  549
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct: 361  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtcccaattt  420


Query: 550  ctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttacccag  609
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  ctaatataacagaaaatatgtacataaatttgacctgctcatctatacacggttacccag  480


Query: 610  aacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggta  669
            |||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481  aacctgagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatggtg  540


Query: 670  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  729
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  ttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctg  600


Query: 730  tttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaaga  789
            |||||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Sbjct: 601  tttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaaga  660


Query: 790  cgcggctttttatcttcacctttctctatagagcttgaggaccctcagcctcccccagacc  849
            |  | |||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  cacagctttatcctcacctttctctatagagcttgaggaccctcagcctcccccagacc  720


Query: 850  acattccttggattacagctgtacttccaacagttattatatgtgtgatggtttttctgtc  909
            ||||  |||||||||||||||||||||||| ||||| ||||||||||||||||| |||||
Sbjct: 721  acatccccttggattacagctgtacttccatcagttgttatatgtgtgatggctttctgtc  780


Query: 910  taattctatggaaatggaagaagaagaagcggcctcgcaactcttataaatgtggaacca  969
            ||||||||||||| ||||||||||||||||||    |||||||||||||||||||||||||
Sbjct: 781  taattctatggaagtggaagaagaagaagcaacctcgcaactcttataaatgtggaacca  840


Query: 970  acacaatggagagggaagagagtgaacagaccaagaaaagagaaaaaatccatatacctg  1029
            ||||||||||||||||||||||||||||||||||    |||||||||||||  || ||||||
Sbjct: 841  acacaatggagagggaagagagtgaacagaccaaaaaaagagaaaaaattaatgtacctg  900


Query: 1030 aaagatctgatgaagcccagcgtgttttttaaaagttcgaagacatcttcatgcgacaaaa  1089
            ||||||||||||||||||||   |||||||||||||| ||||||| ||||||||||||||
Sbjct: 901  aaagatctgatgaagcccaatgtgttttttaaaagtttgaagacaccttcatgcgacaaaa  960


Query: 1090 gtgatacatgtttttaattaaagagtaaagcccatacaagtattcatttttctacccctt  1149
            |||||||| |||||||||||||||||||||||||||||||||||||||| ||| |||||||
Sbjct: 961  gtgatacacgtttttaattaaagagtaaagcccatacaagtattcattcttttacccctt  1020


Query: 1150 tcctttgtaagttcct 1165
            ||||||||||||||||
```

Sbjct: 1021 tcctttgtaagttcct 1036

□ >gi|13649983|gb|AF344836.1|AF344836   Papio cynocephalus anubis CD86 protein precu
            cds
          Length = 901

 Score = 1179 bits (595), Expect = 0.0
 Identities = 667/691 (96%)
 Strand = Plus / Plus

Query: 129 tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 188
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1   tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 60

Query: 189 cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac 248
            || ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 61   cccctgaagattcaagcttatttcaatgagactgcagacctgccatgccagtttgcaaac 120

Query: 249 tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt 308
            |||||||||| |||||||||||||||||||||||||||||||||| | ||||||||||||||
Sbjct: 121 tctcaaaaccgaagcctgagtgagctagtagtattttggcagaatcaggaaaacttggtt 180

Query: 309 ctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggc 368
            |||||||||||||||||||||| ||| |||||||||||| |||||||||||||||||||||
Sbjct: 181 ctgaatgaggtatacttaggcagagaaaaatttgacagcgttcattccaagtatatgggc 240

Query: 369 cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428
            ||||||||||||| |||| ||||||||||||| ||||||| |||||||||||||||||||
Sbjct: 241 cgcacaagttttgatccggagagttggaccctgaggcttcacaaccttcagatcaaggac 300

Query: 429 aagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccac 488
            ||||||||||||||||||||||||||||||||||||| |||||||||||||||| ||||||
Sbjct: 301 aagggcttgtatcaatgtatcatccatcacaaaaaggcccacaggaatgatccgcatccac 360

Query: 489 cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt 548
            ||||||||||||||||||||||||||||||| |||||||||||||||||||||| ||||||
Sbjct: 361 cagatgaattctgaactgtcagtgcttgctagcttcagtcaacctgaaatagtcccaatt 420

Query: 549 tctaatataacagaaaatgtgtacataaatttgacctgctcatctatacacggttaccca 608
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct: 421 tctaatataacagaaaatatgtacataaatttgacctgctcatctatacacggttaccca 480

Query: 609 gaacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggt 668
            ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 481 gaacctgagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatggt 540

Query: 669 attatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 728
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```
Sbjct: 541 gttatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 600


Query: 729 gtttcattccctgatgttacgagcaatatgaccatcttctgtattctggaaactgacaag 788
            ||||||||||||||||||||||||||| |||||||||||||||| |||||||||||||||||
Sbjct: 601 gtttcattccctgatgttacgagcaacatgaccatcttctgtgttctggaaactgacaag 660


Query: 789 acgcggcttttatcttcacctttctctatag 819
            || | ||||||||| ||||||||||||||||||
Sbjct: 661 acacagctttatcctcacctttctctatag 691
```

```
Score =  307 bits (155), Expect = 7e-80
Identities = 191/203 (94%)
Strand = Plus / Plus


Query: 963  ggaaccaacacaatggagagagggaagagagtgaacagaccaagaaaagagaaaaaatccat 1022
            |||||||||||||||||||||||||||||||||||||||||| |||||||||||||  ||
Sbjct: 691  ggaaccaacacaatggagagagggaagagagtgaacagaccaaaaaaagagaaaaaattaat 750


Query: 1023 atacctgaaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgc 1082
            |||||||||||||||||||||||||| ||||||||||||||||| ||||||| ||||||||
Sbjct: 751 gtacctgaaagatctgatgaagcccaatgtgtttttaaaagtttgaagacaccttcatgc 810


Query: 1083 gacaaaagtgatacatgttttttaattaaagagtaaagcccatacaagtattcattttttc 1142
            ||||||||||||| |   ||||||||||||||||||||||||||||||||||||||| ||||
Sbjct: 811 gacaaaagtgatacgcatttttaattaaagagtaaagcccatacaagtattcattctttc 870


Query: 1143 taccctttcctttgtaagttcct 1165
            |||||||||||||||||||||||
Sbjct: 871 taccctttcctttgtaagttcct 893
```


□ >gi|808032|gb|U17722.1|HSB72S8 **L** Human CTLA-4 counter-receptor B7.2 (B7.2) gene,
               cds
          Length = 630

```
Score =  805 bits (406), Expect = 0.0
Identities = 409/410 (99%)
Strand = Plus / Plus


Query: 1008 agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 1067
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 221  agagaaaaaatccatatacctgaaagatctgatgaagcccagcgtgtttttaaaagttcg 280


Query: 1068 aagacatcttcatgcgacaaaagtgatacatgttttttaattaaagagtaaagcccataca 1127
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 281  aagacatcttcatgcgacaaaagtgatacatgttttttaattaaagagtaaagcccataca 340


Query: 1128 agtattcatttttctacccttcctttgtaagttcctgggcaaccttttgatttcttc 1187
```

```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 341  agtattcattttttctacccctttcctttgtaagttcctgggcaaccttttgatttcttc 400


Query: 1188 cagaaggcaaaaagacattaccatgagtaataaggggggctccaggactccctctaagtgg 1247
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 401  cagaaggcaaaaagacattaccatgagtaataaggggggctccaggactccctctaagtgg 460


Query: 1248 aatagcctccctgtaactccagctctgctccgtatgccaagaggagactttaattctctt 1307
        ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct: 461  aatagcctccctgtaactccagctctgctccgtatgacaagaggagactttaattctctt 520


Query: 1308 actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 1367
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 521  actgcttcttttcacttcagagcacacttatgggccaagcccagcttaatggctcatgac 580


Query: 1368 ctggaaataaaatttaggaccaatacctcctccagatcagattcttctct 1417
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 581  ctggaaataaaatttaggaccaatacctcctccagatcagattcttctct 630



[ ]>gi|808028|gb|U17718.1|HSB72S4    Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ε
            Length = 741

 Score =  660 bits (333), Expect = 0.0
 Identities = 336/337 (99%)
 Strand = Plus / Plus


Query: 180  ggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaa 239
        |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 240  ggtgctgctcctctggagattcaagcttatttcaatgagactgcagacctgccatgccaa 299


Query: 240  tttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaa 299
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 300  tttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaa 359


Query: 300  aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 359
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 360  aacttggttctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaag 419


Query: 360  tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 419
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 420  tatatgggccgcacaagttttgattcggacagttggaccctgagacttcacaatcttcag 479


Query: 420  atcaaggacaagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgatt 479
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 480  atcaaggacaagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgatt 539


Query: 480  cgcatccaccagatgaattctgaactgtcagtgcttg 516
        |||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 540 cgcatccaccagatgaattctgaactgtcagtgcttg 576
```

☐ >gi|808029|gb|U17719.1|HSB72S5   Human CTLA-4 counter-receptor B7.2 (B7.2) gene, є
             Length = 737

```
 Score =  603 bits (304), Expect = e-169
 Identities = 304/304 (100%)
 Strand = Plus / Plus
```

```
Query: 516 gctaacttcagtcaacctgaaatagtaccaatttctaatataacagaaaatgtgtacata 575
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 151 gctaacttcagtcaacctgaaatagtaccaatttctaatataacagaaaatgtgtacata 210
```

```
Query: 576 aatttgacctgctcatctatacacggttacccagaacctaagaagatgagtgttttgcta 635
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 211 aatttgacctgctcatctatacacggttacccagaacctaagaagatgagtgttttgcta 270
```

```
Query: 636 agaaccaagaattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtc 695
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 271 agaaccaagaattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtc 330
```

```
Query: 696 acagaactgtacgacgtttccatcagcttgtctgtttcattccctgatgttacgagcaat 755
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 331 acagaactgtacgacgtttccatcagcttgtctgtttcattccctgatgttacgagcaat 390
```

```
Query: 756 atgaccatcttctgtattctggaaactgacaagacgcggcttttatcttcacctttctct 815
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 391 atgaccatcttctgtattctggaaactgacaagacgcggcttttatcttcacctttctct 450
```

```
Query: 816 atag 819
            ||||
Sbjct: 451 atag 454
```

☐ >gi|6572518|gb|AF106827.1|AF106827   Ⓤ Canis familiaris truncated B7-2 protein (CI
             Length = 1795

```
 Score =  396 bits (200), Expect = e-106
 Identities = 502/602 (83%), Gaps = 3/602 (0%)
 Strand = Plus / Plus
```

```
Query: 129 tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 188
            |||||||||| ||||| |||||||||||||||||||| || ||||||||| ||||||||||
Sbjct: 19  tgcactatggaactgaataacattctctttgtgatgaccctcctgctctatggtgctgct 78
```

```
Query: 189 cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac 248
            |  ||||||| |||||||| |||||||||  |||||| |||| ||||||||||||| ||||
Sbjct: 79  tccatgaagagtcaagcatatttcaacaagactggagaactgccatgccattttacaaat 138
```

```
Query:  249  tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt  308
             |||||||||  |||||||  |||| | ||||| |||||||||||||||||| ||  |||||
Sbjct:  139  tctcaaaacataagcctggatgagttggtagtgttttggcaggaccaggataagctggtt  198


Query:  309  ctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggc  368
             ||| | ||| |||||  |||||||||||||  | | | ||||||||  ||||||||| ||||
Sbjct:  199  ctgtacgagctatacagaggcaaagagaaccctcaaaatgttcatcgcaagtataagggc  258


Query:  369  cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac  428
             |||||||| |||||    |||| |||||||||||||||||| || ||| |||||||||||||
Sbjct:  259  cgcacaagctttgacaaagacaattggaccctgagactccataatattcagatcaaggac  318


Query:  429  aagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccac  488
             |||||||||||||||||| || | |||||| ||| ||||| |||| | ||| ||| |||
Sbjct:  319  aagggcttgtatcaatgtttcgttcatcataaagggcccaaaggactcgttcccatgcac  378


Query:  489  cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt  548
             ||||||||||||||| || ||||||||||||||||||||||||||||||||| |   || |
Sbjct:  379  cagatgaattctgacctatcagtgcttgctaacttcagtcaacctgaaataatggtaact  438


Query:  549  tctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttac  605
             ||||||| |||||||||   ||    ||||||||||||||||||||| ||||| ||||||
Sbjct:  439  tctaatagaacagaaaaattctggcatcataaatttgacctgctcatccatacaaggttac  498


Query:  606  ccagaacctaagaagatgagtgtgttttgctaagaaccaagaattcaactatcgagtatgat  665
             ||||||||| ||| |||||  | ||||| ||| |||| |||||||||| ||   ||||||||
Sbjct:  499  ccagaacccaaggagatgtattttttggtaaaaaccgagaattcaagtactaagtatgat  558


Query:  666  ggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttg  725
              | | ||| ||||||||||||||| ||||||||||||||| ||| ||||||| ||||||||
Sbjct:  559  actgtcatgaagaaatctcaaaataatgtcacagaactctacaacgtttctatcagcttg  618


Query:  726  tc  727
             ||
Sbjct:  619  tc  620
```

```
 Score = 67.9 bits (34), Expect = 1e-07
 Identities = 81/96 (84%), Gaps = 3/96 (3%)
 Strand = Plus / Plus
```

```
Query:  1029  gaaagatctgatgaagcccagcgtgtttttaaaagttcgaagacatcttcatgcgacaaa  1088
              |||||||||||||||||||||| |||   |||| | |||||||||| ||||| |||||||
Sbjct:  775   gaaagatctgatgaagcccagtgtg---ttaacatttcgaagacagcttcaggcgacaac  831


Query:  1089  agtgatacatgtttttaattaaagagtaaagcccat  1124
              ||| ||||  |||||||||||||||||||| ||||
```

Sbjct: 832   agtactacacagttttaattaaagagtaaagtccat 867

Score = 60.0 bits (30), Expect = 3e-05
Identities = 169/210 (80%), Gaps = 9/210 (4%)
Strand = Plus / Plus

Query: 1537 actacctcctcagtctgggtgggacttatgtat-ttatgaccttatagtgtt-----aat 1590
             ||||||||| ||||||||||||||| || |||||| |||||| | ||||||||| |||
Sbjct: 1250 actacctctgcagtctgggtgggagttttgtatgttatggctttatagtgttgctttaat 1309

Query: 1591 atcttgaaacatagagatctatgtactgtaatagtgtgattactatgctctagagaaaag 1650
             || |||| |||||| ||| | ||||||| ||||| ||| ||||||||||| || |||||||
Sbjct: 1310 attttgagacataaagagatgtgtactataataatgtaattactatgccct-gagaaaat 1368

Query: 1651 tctaccc-ctgctaaggagttctcatccctctgtcagggtcagtaaggaaaacggtggcc 1709
             ||||||| ||||| |||||| ||| ||||||| ||||||||||| | |||| ||||||
Sbjct: 1369 tctacccactgctgaggagctcttgctcctctgtgagggtcagtacg-aaaatggtggct 1427

Query: 1710 tagggtacaggcaacaatgagcagaccaac 1739
             | | || | | |||||||||||||||||||||
Sbjct: 1428 tggtgtgctgacaacaatgagcagaccaac 1457

Score = 58.0 bits (29), Expect = 1e-04
Identities = 32/33 (96%)
Strand = Plus / Plus

Query: 1776 cctggagccacttctatctgggctgttgctaat 1808
             |||||||||||||||||||||||||| |||||||
Sbjct: 1506 cctggagccacttctatctgggctgctgctaat 1538

Score = 50.1 bits (25), Expect = 0.026
Identities = 34/37 (91%)
Strand = Plus / Plus

Query: 1308 actgcttcttttcacttcagagcacacttatgggcca 1344
             ||||||||||||| |||||||||||||| |||||||
Sbjct: 1029 actgcttcttttcatctcagagcacacttgtgggcca 1065

☐ >gi|6572516|gb|AF106826.1|AF106826 L U G Canis familiaris B7-2 protein (CD86) mf
         Length = 1897

Score = 396 bits (200), Expect = e-106
Identities = 502/602 (83%), Gaps = 3/602 (0%)
Strand = Plus / Plus

```
Query:  129  tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct  188
             |||||||||  ||||| |||||||||||||||||||| ||  ||||||||| |||||||||
Sbjct:  18   tgcactatggaactgaataacattctctttgtgatgaccctcctgctctatggtgctgct  77


Query:  189  cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac  248
             |  ||||||| ||||||| |||||||||  ||||||  ||| ||||||||||||| |||||
Sbjct:  78   tccatgaagagtcaagcatatttcaacaagactggagaactgccatgccattttacaaat  137


Query:  249  tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt  308
             ||||||||| |||||||  |||| | ||||| |||||||||||||||||||| || |||||
Sbjct:  138  tctcaaaacataagcctggatgagttggtagtgttttggcaggaccaggataagctggtt  197


Query:  309  ctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggc  368
             ||| | ||| |||||  |||||||||||| |  | |||||||  ||||||||||| ||||
Sbjct:  198  ctgtacgagctatacagaggcaaagagaaccctcaaaatgttcatcgcaagtataagggc  257


Query:  369  cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac  428
             ||||||||| |||||  ||||  |||||||||||||||| ||  ||| ||||||||||||
Sbjct:  258  cgcacaagctttgacaaagacaattggaccctgagactccataatattcagatcaaggac  317


Query:  429  aagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccac  488
             |||||||||||||||||| || | ||||| ||| |||||  ||||| |||| ||| |||
Sbjct:  318  aagggcttgtatcaatgtttcgttcatcataaagggcccaaaggactcgttcccatgcac  377


Query:  489  cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt  548
             ||||||||||||| || ||||||||||||||||||||||||||||||||||| |  || |
Sbjct:  378  cagatgaattctgacctatcagtgcttgctaacttcagtcaacctgaaataatggtaact  437


Query:  549  tctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttac  605
             ||||||| |||||||||  ||  ||||||||||||||||||||||||||| ||||| |||||
Sbjct:  438  tctaatagaacagaaaattctggcatcataaatttgacctgctcatccatacaaggttac  497


Query:  606  ccagaacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgat  665
             |||||||| ||| ||||| | ||||| ||| |||||  ||||||||| ||    |||||||
Sbjct:  498  ccagaacccaaggagatgtatttttggtaaaaccgagaattcaagtactaagtatgat  557


Query:  666  ggtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttg  725
              | | ||| ||||||||||| ||||||||||||||||| ||| |||||||| ||||||||||
Sbjct:  558  actgtcatgaagaaatctcaaaataatgtcacagaactctacaacgtttctatcagcttg  617


Query:  726  tc  727
             ||
Sbjct:  618  tc  619
```

```
 Score = 75.8 bits (38), Expect = 5e-10
 Identities = 157/196 (80%), Gaps = 3/196 (1%)
 Strand = Plus / Plus
```

```
Query:  929  gaagaagaagcggcctcgcaactcttataaatgtggaaccaacacaatggagagggaaga  988
             |||||||||| |||| || |||| || |||||| |||||||| | ||||||| ||||
Sbjct:  821  gaagaagaagcagcctggcccctctcatgaatgtgaaaccaacaaagtggagagaaaaga  880


Query:  989  gagtgaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaagccca  1048
             ||||| |||||||||| |||||| |     |||| | | |||||||||||||||||||||
Sbjct:  881  aagtgagcagaccaaggaaagagtacggtaccatgaaacggaaagatctgatgaagccca  940


Query: 1049  gcgtgttttaaaagttcgaagacatcttcatgcgacaaaagtgatacatgttttaatt  1108
             | ||||    || | |||||||||| ||||| ||||||| |||  |||   ||||||||
Sbjct:  941  gtgtgtt---aacatttcgaagacagcttcaggcgacaacagtactacacagttttaatt  997


Query: 1109  aaagagtaaagcccat  1124
             |||||||||| ||||
Sbjct:  998  aaagagtaaagtccat  1013


 Score = 60.0 bits (30), Expect = 3e-05
 Identities = 169/210 (80%), Gaps = 9/210 (4%)
 Strand = Plus / Plus


Query: 1537  actacctcctcagtctgggtggggacttatgtat-ttatgaccttatagtg-----ttaat  1590
             ||||||||  ||||||||||||||||| || ||||| |||||| | |||||||     |||||
Sbjct: 1396  actacctctgcagtctgggtgggagttttgtatgttatggctttatagtgttgctttaat  1455


Query: 1591  atcttgaaacatagagatctatgtactgtaatagtgtgattactatgctctagagaaaag  1650
             || |||| ||||| ||| | |||||| ||||| ||| |||||||||| || |||||||
Sbjct: 1456  attttgagacataaagagatgtgtactataataatgtaattactatgccct-gagaaaat  1514


Query: 1651  tctaccc-ctgctaaggagttctcatccctctgtcagggtcagtaaggaaaacggtggcc  1709
             ||||||| ||||| ||||| ||||| |||       ||||||| ||||||||| | ||||| ||||||
Sbjct: 1515  tctacccactgctgaggagctcttgctcctctgtgagggtcagt-acgaaaatggtggct  1573


Query: 1710  tagggtacaggcaacaatgagcagaccaac  1739
             | | || | | ||||||||||||||||||||
Sbjct: 1574  tggtgtgctgacaacaatgagcagaccaac  1603


 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 32/33 (96%)
 Strand = Plus / Plus


Query: 1776  cctggagccacttctatctgggctgttgctaat  1808
             ||||||||||||||||||||||||| |||||||
Sbjct: 1652  cctggagccacttctatctgggctgctgctaat  1684


 Score = 50.1 bits (25), Expect = 0.026
```

```
Identities = 34/37 (91%)
Strand = Plus / Plus
```

```
Query: 1308 actgcttcttttcacttcagagcacacttatgggcca 1344
            |||||||||||||| |||||||||||||| |||||||
Sbjct: 1175 actgcttcttttcatctcagagcacacttgtgggcca 1211
```

□ >gi|5381423|gb|AF157827.1|AF157827   Felis catus CD86 antigen (CD86) mRNA, complet
         Length = 1138

```
Score =  361 bits (182), Expect = 5e-96
Identities = 508/616 (82%), Gaps = 3/616 (0%)
Strand = Plus / Plus
```

```
Query: 130  gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189
            |||||||||||||||||| ||| |||| |||||||||||| ||||||||||||||||| | ||
Sbjct: 79   gcactatgggactgagtcacactctccttgtgatggccctcctgctctctggtgtttctt 138
```

```
Query: 190  ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249
            |  |||||| |||||| ||||||||  |||||| ||| ||||||||||||| ||| ||||||
Sbjct: 139  ccatgaagagtcaagcatatttcaacaagactggagaactgccatgccattttacaaact 198
```

```
Query: 250  ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309
            ||||||||  |||||| |||||| ||||||||||||||||||||||||||| || ||||||
Sbjct: 199  ctcaaaacataagcctggatgagctggtagtattttggcaggaccaggataagctggttc 258
```

```
Query: 310  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369
            || |||||| ||| |  |||||||||||||  |  |  |||||||||| ||| |||| ||||||
Sbjct: 259  tgtatgagatattcagaggcaaagagaaccctcaaaatgttcatctcaaatataagggcc 318
```

```
Query: 370  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429
            | |||||| |||||     |||||| ||||||||||||||| |||||| |||||||||||||||
Sbjct: 319  gtacaagctttgacaaggacaactggaccctgagactccacaatgttcagatcaaggaca 378
```

```
Query: 430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489
            |||||    ||||| ||| |||| ||| | ||| |||||| |||| | ||| ||| ||||
Sbjct: 379  agggcacatatcactgtttcattcattataaagggcccaaaggactagttcccatgcacc 438
```

```
Query: 490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt 549
            | |||| |||||| || ||||||||||||||||||||||||||||||||||  | || || 
Sbjct: 439  aaatgagttctgacctatcagtgcttgctaacttcagtcaacctgaaataacagtaactt 498
```

```
Query: 550  ctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttacc 606
            ||||||| ||||||||   ||    ||||||||||||||||||||||||||||  |||||||
Sbjct: 499  ctaatagaacagaaaattctggcatcataaatttgacctgctcatctatacaaggttacc 558
```

```
Query: 607  cagaacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatg 666
            |||||||||| |||||  |  |  ||||| ||  ||||||||||     ||||||||
```

```
Sbjct: 559 cagaacctaaggagatgtattttcagctaaacactgagaattcaactactaagtatgata 618


Query: 667 gtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgt 726
            | |  ||| ||||||||||| |||||||| |||||||||||| ||||||| |||||||||
Sbjct: 619 ctgtcatgaagaaatctcaaaataatgtgacagaactgtacaacgtttctatcagcttgc 678


Query: 727 ctgtttcattccctga 742
            || ||||| |||||||
Sbjct: 679 ctttttcagtccctga 694



 Score = 54.0 bits (27), Expect = 0.002
 Identities = 102/127 (80%)
 Strand = Plus / Plus


Query: 929  gaagaagaagcggcctcgcaactcttataaatgtggaaccaacacaatggagagggaaga 988
            |||||||||| |||| || |||| || |||||| |||| || || |||||   ||||
Sbjct: 887  gaagaagaagcagcctggcccctctcatgaatgtgaaaccatcaaaagggagagaaaaga 946


Query: 989  gagtgaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaagccca 1048
            |||  |||||||||| ||||||  |  |  ||| |||||||| ||||||||||||||||||
Sbjct: 947  gagcaaacagaccaacgaaagagtaccataccacgtacctgagagatctgatgaagccca 1006


Query: 1049 gcgtgtt 1055
            | ||||||
Sbjct: 1007 gtgtgtt 1013




   >gi|15418725|gb|AY007704.1|   Felis catus CD86 (CD86) mRNA, complete cds
            Length = 2830

 Score =  361 bits (182), Expect = 5e-96
 Identities = 508/616 (82%), Gaps = 3/616 (0%)
 Strand = Plus / Plus


Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189
            ||||||||||||||||||| ||| |||| |||||||||| ||||||||||||| || | ||
Sbjct: 195 gcactatgggactgagtcacactctccttgtgatggccctcctgctctctggtgtttctt 254


Query: 190 ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249
            |   |||||| ||||||| ||||||||| |||||| ||| |||||||||||| ||| |||||
Sbjct: 255 ccatgaagagtcaagcatatttcaacaagactggagaactgccatgccattttacaaact 314


Query: 250 ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309
            |||||||| ||||||| |||||| ||||||||||||||||||||||||| || |||||||
Sbjct: 315 ctcaaaacataagcctggatgagctggtagtattttggcaggaccaggataagctggttc 374


Query: 310 tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc 369
            || ||||| ||| |  |||||||||||| | | | ||||||| ||| |||| |||||
```

```
Sbjct: 375  tgtatgagatattcagaggcaaagagaaccctcaaaatgttcatctcaaatataagggcc 434


Query: 370  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca 429
            |  |||||  |||||     |||||  ||||||||||||||| ||||||  ||||||||||||
Sbjct: 435  gtacaagctttgacaaggacaactggaccctgagactccacaatgttcagatcaaggaca 494


Query: 430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc 489
            |||||  |||||| ||| |||| ||| | ||| ||||| |||| |  ||| ||| ||||
Sbjct: 495  agggcacatatcactgtttcattcattataaagggcccaaaggactagttcccatgcacc 554


Query: 490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt 549
            | ||||  |||||| ||  ||||||||||||||||||||||||||||||||||  |  || || 
Sbjct: 555  aaatgagttctgacctatcagtgcttgctaacttcagtcaacctgaaataacagtaactt 614


Query: 550  ctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttacc 606
            |||||| ||||||||||   ||     |||||||||||||||||||||||||||  |||||||
Sbjct: 615  ctaatagaacagaaaattctggcatcataaatttgacctgctcatctatacaaggttacc 674


Query: 607  cagaacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatg 666
            |||||||||||| |||||  |  || |  ||||| ||  |||||||||||     |||||||||
Sbjct: 675  cagaacctaaggagatgtatttcagctaaacactgagaattcaactactaagtatgata 734


Query: 667  gtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgt 726
            |  |  ||| ||||||||||| |||||| ||||||||||| ||||||| |||||||||||
Sbjct: 735  ctgtcatgaagaaatctcaaaataatgtgacagaactgtacaacgtttctatcagcttgc 794


Query: 727  ctgtttcattccctga 742
            || ||||| |||||||
Sbjct: 795  ctttttcagtccctga 810



  Score = 99.6 bits (50), Expect = 3e-17
  Identities = 146/177 (82%), Gaps = 2/177 (1%)
  Strand = Plus / Plus


Query: 2054  agcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggtggt 2113
             ||||||||| | || |||||||||||| ||||  |||||||||||||| | ||  ||||||
Sbjct: 2117  agcaacaggtagacagtctgtccaaaaggacttaagacagacagcagctcccatggtggt 2176


Query: 2114  cagggaggggttttggtgatacccaagttattgggatgt--catcttcctggaagcagag 2171
             | ||| |||| | ||| ||| |||||||||||  |||| ||||| ||| | |||||||
Sbjct: 2177  tggtgagaagtttggataataatcaagttattgtgatgtttcatctggctgcaggcagag 2236


Query: 2172  ctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttaggact 2228
             | |||||||| |||||  ||| |||| |||||||||||||||| |||||||||| ||||||||||
Sbjct: 2237  caggggaggaagagctatcatcttgataatgggataaatggaaggaagcttaggact 2293
```

```
Score = 61.9 bits (31), Expect = 7e-06
Identities = 156/197 (79%), Gaps = 3/197 (1%)
Strand = Plus / Plus


Query: 929   gaagaagaagcggcctcgcaactcttataaatgtggaaccaacacaatggagagggaaga 988
             |||||||||| |||| || |||| || |||||| |||||| || || ||||||  ||||
Sbjct: 1003  gaagaagaagcagcctggcccctctcatgaatgtgaaaccatcaaaagggagagaaaaga 1062


Query: 989   gagtgaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaagccca 1048
             |||  |||||||||| |||||| |  |  ||| |||||||  ||||||||||||||||||
Sbjct: 1063  gagcaaacagaccaacgaaagagtaccataccacgtacctgagagatctgatgaagccca 1122


Query: 1049  gcgtgtttttaaaagttcgaagacatcttcatgcgacaaaagtgatacatgtttttaatt 1108
             | || ||   || | || |||||| | ||| ||||||||||| ||||  |||||||||||
Sbjct: 1123  gtgtatt---aacattttgaagacagcctcaggcgacaaaagtactacacatttttaatt 1179


Query: 1109  aaagagtaaagcccata 1125
             ||||| ||||| |||||
Sbjct: 1180  aaagaataaagtccata 1196



Score = 50.1 bits (25), Expect = 0.026
Identities = 46/53 (86%)
Strand = Plus / Plus


Query: 1586  ttaatatcttgaaacatagagatctatgtactgtaatagtgtgattactatgc 1638
             ||||||||||||||||||||| |||   | ||||||| ||||| ||| |||||||||||
Sbjct: 1644  ttaatatcttgaaacataaagagatgtgtactataataatgtaattactatgc 1696



☐ >gi|9796387|dbj|AB030652.1|    Felis catus mRNA for B-lymphocyte activation antiger
           complete cds
         Length = 1270

Score =  361 bits (182), Expect = 5e-96
Identities = 508/616 (82%), Gaps = 3/616 (0%)
Strand = Plus / Plus


Query: 130   gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgctc 189
             ||||||||||||||||||| ||| |||| ||||||||| ||||||||||||||||| | ||
Sbjct: 256   gcactatgggactgagtcacactctccttgtgatggccctcctgctctctggtgtttctt 315


Query: 190   ctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaact 249
             | ||||||| ||||||| ||||||| ||||| ||| ||||||||.|||||| ||| ||||||
Sbjct: 316   ccatgaagagtcaagcatatttcaacaagactggagaactgccatgccattttacaaact 375


Query: 250   ctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttc 309
             |||||||| ||||||| |||||| ||||||||||||||||||||||||| || |||||||
Sbjct: 376   ctcaaaacataagcctggatgagctggtagtattttggcaggaccaggataagctggttc 435
```

```
Query:  310  tgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggcc  369
             || |||||| ||| |  |||||||||||||   | | | ||||||||  ||| |||| |||||
Sbjct:  436  tgtatgagatattcagaggcaaagagaaccctcaaaatgttcatctcaaatataagggcc  495


Query:  370  gcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggaca  429
             | |||||| |||||     |||||  ||||||||||||| ||||||  ||||||||||||||
Sbjct:  496  gtacaagctttgacaaggacaactggaccctgagactccacaatgttcagatcaaggaca  555


Query:  430  agggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccacc  489
             |||||     |||||| ||| |||| ||| | |||  ||||| |||| |  ||| ||| ||||
Sbjct:  556  agggcacatatcactgtttcattcattataaagggcccaaaggactagttcccatgcacc  615


Query:  490  agatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaattt  549
             | ||||| |||||| || ||||||||||||||||||||||||||||||||||   |  || ||
Sbjct:  616  aaatgagttctgacctatcagtgcttgctaacttcagtcaacctgaaataacagtaactt  675


Query:  550  ctaatataacagaaaa---tgtgtacataaatttgacctgctcatctatacacggttacc  606
             ||||||  |||||||| |  ||         ||||||||||||||||||||||||  |||||||
Sbjct:  676  ctaatagaacagaaaattctggcatcataaatttgacctgctcatctatacaaggttacc  735


Query:  607  cagaacctaagaagatgagtgtttttgctaagaaccaagaattcaactatcgagtatgatg  666
             ||||||||||| |||||   | ||  |||||  ||     |||||||||||    ||||||||
Sbjct:  736  cagaacctaaggagatgtattttcagctaaacactgagaattcaactactaagtatgata  795


Query:  667  gtattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgt  726
             | | ||| |||||||||||| ||||||| |||||||||||||| |||||| ||||||||| 
Sbjct:  796  ctgtcatgaagaaatctcaaaataatgtgacagaactgtacaacgtttctatcagcttgc  855


Query:  727  ctgtttcattccctga  742
             || |||||| |||||||
Sbjct:  856  cttttcagtccctga  871



  Score = 69.9 bits (35), Expect = 3e-08
  Identities = 157/197 (79%), Gaps = 3/197 (1%)
  Strand = Plus / Plus


Query:  929   gaagaagaagcggcctcgcaactcttataaatgtggaaccaacacaatggagagggaaga  988
             ||||||||||| |||| || ||    |||| || |||||| ||||| || || |||||| ||||
Sbjct:  1064  gaagaagaagcagcctggcccctctcatgaatgtgaaaccatcaaaagggagagaaaaga  1123


Query:  989   gagtgaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaagccca  1048
             |||   ||||||||| |||||| |  |   ||| ||||||| |||||||||||||||||||||
Sbjct:  1124  gagcaaacagaccaacgaaagagtaccataccacgtacctgagagatctgatgaagccca  1183


Query:  1049  gcgtgtttttaaaagttcgaagacatcttcatgcgacaaaagtgatacatgtttttaatt  1108
             | |||     |||| | || |||||||| ||| | |||||||||| |||| |||||||||||
Sbjct:  1184  gtgtgtttttaaaagtt---gaagacagcctcaggcgacaaaagtactacacatttttaatt  1240
```

```
Query: 1109 aaagagtaaagcccata 1125
             |||||| ||||| |||||
Sbjct: 1241 aaagaataaagtccata 1257
```

□ >gi|755098|dbj|D49842.1|RABCD86B   Oryctolagus cuniculus mRNA for CD86, complete (
            Length = 1156

 Score = 355 bits (179), Expect = 3e-94
 Identities = 493/595 (82%), Gaps = 2/595 (0%)
 Strand = Plus / Plus

```
Query: 129  tgcactatgggactgagtaacattctctttgtgatggccttcctgctctctggtgctgct 188
            ||||| ||||||||||||  ||    |||||||||||||| |||||||||||||||||||||
Sbjct: 19   tgcacaatgggactgagtgtcacggtcttgtgatggccctcctgctctctggtgctgct 78


Query: 189  cctctgaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaac 248
            | || | ||| || |||||||||| ||||||||||||||||||||||||| ||| |||||
Sbjct: 79   tcccttaggatacaggcttatttcaacaagactgcagacctgccatgccagtttacaaac 138


Query: 249  tctcaaaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggtt 308
            ||||||| |  |||||| ||||||||| ||||||||||||||||||||||||| |  ||||||
Sbjct: 139  tctcaaagcagaagcctaagtgagctggtagtattttggcaggaccaggagaggttggtt 198


Query: 309  ctgaatgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggc 368
            ||| | ||| | | ||||||||| |||||||  |||||| ||| || | | ||||| || |||
Sbjct: 199  ctgtacgagctcttcttaggcagagagaaacctgacaatgtggatcctaagtacattggc 258


Query: 369  cgcacaagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggac 428
            |||||||| ||||| |||   |||  ||||||||| |||   |||||||||| ||||||||||
Sbjct: 259  cgcacaagctttgaccaggaaagttggaacctacaacttcacaacgttcagatcaaggac 318


Query: 429  aagggcttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccac 488
            ||||||  |||||||||| |   |||||||| | | ||| |||  || ||| |||| ||  ||
Sbjct: 319  aagggcgtgtatcaatgttttgtccatcacagaggggccaaagggctggttcccatctac 378


Query: 489  cagatgaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatt 548
            |||||||||||||| ||||||||||||||||| ||||| ||||||| ||||||| |  ||||
Sbjct: 379  cagatgaattctgagctgtcagtgcttgctaatttcactcaaccggaaataacattaatt 438


Query: 549  tctaatataaca-gaaaatgtgtacataaatttgacctgctcatctatacacggttaccc 607
            || ||||||||| |||| | |||  |||||||||||||||||| || | | ||||| |||||
Sbjct: 439  tccaatataacaagaaaattctgc-cataaatttgacctgctcgtctgtacaaggctaccc 497


Query: 608  agaacctaagaagatgagtgttttgctaagaaccaagaattcaactatcgagtatgatgg 667
            ||||||||||||||||||||  || ||| |||  ||||| |||| | | |||||||||||||
Sbjct: 498  agaacctaagaagatgttctttgtgctaaaaactgagaatgcaaccactgagtatgatgg 557
```

```
Query: 668 tattatgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagc 722
            | | || |||||||||||||||||||||||||| ||||||| || |||||||||||
Sbjct: 558 tgtcatcgagaaatctcaagataatgtcacaggactgtacaacatttccatcagc 612
```

☐ >gi|808030|gb|U17720.1|HSB72S6   Human CTLA-4 counter-receptor B7.2 (B7.2) gene, €
          Length = 571

 Score = 293 bits (148), Expect = 1e-75
 Identities = 148/148 (100%)
 Strand = Plus / Plus

```
Query: 817 tagagcttgaggaccctcagcctcccccagaccacattccttggattacagctgtacttc 876
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 167 tagagcttgaggaccctcagcctcccccagaccacattccttggattacagctgtacttc 226
```

```
Query: 877 caacagttattatatgtgtgatggttttctgtctaattctatggaaatggaagaagaaga 936
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 227 caacagttattatatgtgtgatggttttctgtctaattctatggaaatggaagaagaaga 286
```

```
Query: 937 agcggcctcgcaactcttataaatgtgg 964
            ||||||||||||||||||||||||||||
Sbjct: 287 agcggcctcgcaactcttataaatgtgg 314
```

☐ >gi|47523527|ref|NM_214222.1| 🄻🅄 Sus scrofa CD86 protein (CD86), mRNA
          Length = 994

 Score = 264 bits (133), Expect = 9e-67
 Identities = 398/481 (82%), Gaps = 4/481 (0%)
 Strand = Plus / Plus

```
Query: 135 atgggactgagtaacattctctttgtgatggccttcctgctctctggtgctg-ctcctct 193
            ||||||||||||||||||||||||||||||||||||||| | |||||||||||||||| |
Sbjct: 1   atgggactgagtaacattctctttgtgatggtcctcctgctctctggtgctgcctcct-t 59
```

```
Query: 194 gaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctca 253
            ||| | ||| || |||||||||||||||||| ||| ||||| ||||| ||| |||||| ||
Sbjct: 60  gaaaagtcaggcatatttcaatgagactggagaactgccgtgccattttacaaactcgca 119
```

```
Query: 254 aaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaa 313
            |||| |||||||| ||||| || |||||||||||||||||||| ||| |||||||| |
Sbjct: 120 gaacctaagcctggatgagctggtcatattttggcaggaccaggataacctggttctcta 179
```

```
Query: 314 tgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcac 373
            ||| |||||| |||| ||||||| | | | ||||| |||||||||||||||||| |||||
Sbjct: 180 cgagctataccgaggccaagagaagcctcataatgttaattccaagtatatgggtcgcac 239
```

```
Query: 374  aagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaaggg 433
            ||| |||||    || ||  |||||||||||||||| |||||  |||| |||||||||||||
Sbjct: 240  aagctttgaccaggccacctggaccctgagactccacaacgttcaaatcaaggacaaggg 299


Query: 434  cttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccaccagat 493
            ||  |||||||||| |||||||||| |||   ||      ||| | |||| |||||||||||
Sbjct: 300  ctcatatcaatgtttcatccatcataaagggccgcatggacttgttcctatccaccagat 359


Query: 494  gaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttctaa 553
            || ||||||| || ||| ||||||||||||||||||||||||||||||    | | || |||
Sbjct: 360  gagttctgacctatcattgcttgctaacttcagtcaacctgaaataaacctacttactaa 419


Query: 554  tataacagaaaa-tgtgtacataaatttgacctgctcatctatacacggttacccagaac 612
            |    |||||||| | |||  |||||||||||||||||||||||||| ||| || ||||||||
Sbjct: 420  tcacacagaaaattctgt-cataaatttgacctgctcatctacacaaggctacccagaac 478


Query: 613  c 613
            |
Sbjct: 479  c 479
```

☐ >gi|2198558|gb|L76099.1|PIGCD86G **L U** Sus scrofa CD86 mRNA, complete cds
              Length = 994

 Score = 264 bits (133), Expect = 9e-67
 Identities = 398/481 (82%), Gaps = 4/481 (0%)
 Strand = Plus / Plus

```
Query: 135  atgggactgagtaacattctctttgtgatggccttcctgctctctggtgctg-ctcctct 193
            |||||||||||||||||||||||||||||||||||| | |||||||||||||||| ||||| |
Sbjct: 1    atgggactgagtaacattctctttgtgatggtcctcctgctctctggtgctgcctcct-t 59


Query: 194  gaagattcaagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctca 253
            ||| | ||| || ||||||||||||||||| ||| |||||| |||||| ||| |||||| ||
Sbjct: 60   gaaaagtcaggcatatttcaatgagactggagaactgccgtgccattttacaaactcgca 119


Query: 254  aaaccaaagcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaa 313
            |||| |||||||  |||||| ||  |||||||||||||||||||| ||| ||||||| |
Sbjct: 120  gaacctaagcctggatgagctggtcatattttggcaggaccaggataacctggttctcta 179


Query: 314  tgaggtatacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcac 373
            ||| |||||  |||| |||||||  | | | |||| ||||||||||||||||||| |||||
Sbjct: 180  cgagctataccgaggccaagagaagcctcataatgttaattccaagtatatgggtcgcac 239


Query: 374  aagttttgattcggacagttggaccctgagacttcacaatcttcagatcaaggacaaggg 433
            ||| |||||    || ||  |||||||||||||||| |||||  |||| |||||||||||||
Sbjct: 240  aagctttgaccaggccacctggaccctgagactccacaacgttcaaatcaaggacaaggg 299


Query: 434  cttgtatcaatgtatcatccatcacaaaaagcccacaggaatgattcgcatccaccagat 493
```

```
            ||  |||||||||| ||||||||||| ||| |||    ||| | |||  ||||||||||||
Sbjct: 300  ctcatatcaatgtttcatccatcataaagggccgcatggacttgttcctatccaccagat 359


Query: 494  gaattctgaactgtcagtgcttgctaacttcagtcaacctgaaatagtaccaatttctaa 553
            || ||||||| || ||| |||||||||||||||||||||||||||    | | || ||||
Sbjct: 360  gagttctgacctatcattgcttgctaacttcagtcaacctgaaataaacctacttactaa 419


Query: 554  tataacagaaaa-tgtgtacataaatttgacctgctcatctatacacggttacccagaac 612
            |     |||||||| | |||  ||||||||||||||||||||||||| ||| || |||||||||
Sbjct: 420  tcacacagaaaattctgt-cataaatttgacctgctcatctacacaaggctacccagaac 478


Query: 613  c 613
            |
Sbjct: 479  c 479




☐ >gi|808025|gb|U17715.1|HSB72S1    Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ɛ
            Length = 478

 Score =  258 bits (130), Expect = 6e-65
 Identities = 130/130 (100%)
 Strand = Plus / Plus


Query: 1    ggaaggcttgcacagggtgaaagctttgcttctctgctgctgtaacagggactagcacag 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 163  ggaaggcttgcacagggtgaaagctttgcttctctgctgctgtaacagggactagcacag 222


Query: 61   acacacggatgagtggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 223  acacacggatgagtggggtcatttccagatattaggtcacagcagaagcagccaaaatgg 282


Query: 121  atccccagtg 130
            ||||||||||
Sbjct: 283  atccccagtg 292




☐ >gi|10803379|emb|AJ291475.1|BTA291475   🅛🅤 Bos taurus partial mRNA for CD86 antiɡ
            Length = 924

 Score =  153 bits (77), Expect = 2e-33
 Identities = 334/418 (79%), Gaps = 5/418 (1%)
 Strand = Plus / Plus


Query: 210  ttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaaagcctgagt 269
            ||||| |||||||| ||| ||||||||||| ||| |||||| | ||||||| ||||||
Sbjct: 186  ttcaacgagactggagaactgccatgccactttccaaacacccaaaacctcagcctggac 245


Query: 270  gagctagtagtatttttggcaggaccaggaaaacttggttctgaatgaggtatacttaggc 329
            || || || |||||||||||| ||| | || |||||||  ||||| ||| | |  ||||
```

```
Sbjct: 246 gaactggtgatattttggcaggatcagaataagttggttctttatgagctattcaaaggc 305


Query: 330 aaagagaaatttgacagtgttcattccaagtatatgggccgcacaagttttgattcggac 389
            |||||||     | | |||| || |||||||||| ||||||||||| |||||    ||||
Sbjct: 306 caagagaagcccaataatgttaatcccaagtatataggccgcacaagctttgaccaggac 365


Query: 390 agttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtatcaatgtatc 449
            ||||||||| ||||||| |||||   |||| ||||| |||| ||||  |||||||||| ||
Sbjct: 366 agttggaccttgagactccacaacgttcaaatcaaagacacaggctcgtatcaatgtttc 425


Query: 450 atccatcacaaaaagcccacaggaatgattcgcatccaccagatgaattctgaactgtca 509
            ||||||||  |  ||  | ||  |||| || || |||||||||||||| ||||||  ||  |
Sbjct: 426 atccatcatagaaggtcccaaggattggtttccatccaccagatgagttctgacctgata 485


Query: 510 gtgcttgctaacttcagtcaacctgaaatagtaccaatttctaatataacagaaaatgtg 569
            |||||  |||||||||||||||||  |||||||  || |||| ||||    ||||||||| ||
Sbjct: 486 gtgctggctaacttcagtcaaccagaaataagactaattgctaaccaaacagaaaa-gtc 544


Query: 570 ta----cataaatttgacctgctcatctatacacggttacccagaacctaagaagatg 623
            ||    ||| ||||||||||||||||||||||||| ||||||||||||| ||| ||||
Sbjct: 545 taacatcatcaatttgacctgctcatctatacaaggttacccagaacctcagaggatg 602



 Score = 42.1 bits (21), Expect = 6.3
 Identities = 45/53 (84%)
 Strand = Plus / Plus


Query: 676 agaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtct 728
            ||||||||||  |||| ||||||||||| ||| | ||||| |||||| |||||
Sbjct: 655 agaaatctcaaagtaatatcacagaactatacaatgtttctatcagcgtgtct 707



□ >gi|40217708|gb|AC117662.13| Ⓓ Mus musculus chromosome 16, clone RP23-351D19, cc
           Length = 293822

 Score =  143 bits (72), Expect = 2e-30
 Identities = 198/240 (82%)
 Strand = Plus / Minus


Query: 201    caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
              |||||||||||||||| ||||||| | ||||| |||| |||| |||| |||||||||| |
Sbjct: 100828 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 100769


Query: 261    agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
              |||||||||||||| |||||||||||||||||||| |||| |||||||||| | |||
Sbjct: 100768 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 100709


Query: 321    tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
              || || |||| ||||||| |||| ||||| || || |||||||||| |||
```

```
Sbjct: 100708 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 100649


Query: 381    gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
              ||   | ||| ||||| ||  |||||||||||| ||||||||||||||| |||||  ||||
Sbjct: 100648 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 100589



  Score = 58.0 bits (29), Expect = 1e-04
  Identities = 53/61 (86%)
  Strand = Plus / Minus


Query: 645    aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
              .||||||||| ||||||| || ||  ||||||| ||| ||||||||||||||||||||||||
Sbjct: 98313  aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 98254


Query: 705    t 705
              |
Sbjct: 98253  t 98253
```

□ >gi|4587845|gb|AF065900.1|AF065900 **L U** Mus musculus strain SJL/J CD86 antigen ((
         Length = 984

```
  Score =  143 bits (72), Expect = 2e-30
  Identities = 198/240 (82%)
  Strand = Plus / Plus


Query: 201  caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
            |||||||||||||||||| |||||| | |||||| |||| |||| |||| ||||||||| |
Sbjct: 117  caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 176


Query: 261  agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
            ||||||||||||||| ||||||||||||||||||||| |||| |||||||| | |||
Sbjct: 177  agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 236


Query: 321  tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
            || || |||| |||||||| |||| ||||| || ||||||| |||||||||| || |||
Sbjct: 237  tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 296


Query: 381  gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
            ||   | ||| ||||| ||  |||||||||||| ||||||||||||||| |||||  ||||
Sbjct: 297  gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 356



  Score = 58.0 bits (29), Expect = 1e-04
  Identities = 53/61 (86%)
  Strand = Plus / Plus


Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
```

```
              ||||||||||  |||||||| || ||  ||||||||| |||  |||||||||||||||||||||
Sbjct: 555 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 614


Query: 705 t 705
              |
Sbjct: 615 t 615



 Score = 46.1 bits (23), Expect = 0.41
 Identities = 35/39 (89%)
 Strand = Plus / Plus


Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
              ||||||||||||| | || |||||||||| |||||||||||
Sbjct: 417 gaactgtcagtgatcgccaacttcagtgaacctgaaata 455



 □ >gi|4587843|gb|AF065899.1|AF065899   [L][U][G]  Mus musculus strain B10.S/J CD86 antige
              Length = 984

 Score =  143 bits (72), Expect = 2e-30
 Identities = 198/240 (82%)
 Strand = Plus / Plus


Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
              ||||||||||||||||||||| ||||||| | ||||| |||| |||| |||| |||||||| |
Sbjct: 117 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 176


Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
              |||||||||||||| |||||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 177 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 236


Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
              || || |||| |||||||| |||| ||||| || ||||||| |||||||||| || |||
Sbjct: 237 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 296


Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
              ||   | ||| |||||| || |||||||||| |||||||||||||| ||||| ||||
Sbjct: 297 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 356



 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 53/61 (86%)
 Strand = Plus / Plus


Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
              ||||||||| |||||||| || || ||||||| |||  ||||||||||||||||||||||
Sbjct: 555 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 614
```

```
Query: 705 t 705
            |
Sbjct: 615 t 615
```

```
Score = 46.1 bits (23), Expect = 0.41
Identities = 35/39 (89%)
Strand = Plus / Plus
```

```
Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
            |||||||||||| |  ||  ||||||||||  ||||||||||
Sbjct: 417 gaactgtcagtgatcgccaacttcagtgaacctgaaata 455
```

☐ >gi|4587841|gb|AF065898.1|AF065898 **L** **U** Mus musculus strain C57BL/6J CD86 antiger
          Length = 984

```
Score =  143 bits (72), Expect = 2e-30
Identities = 198/240 (82%)
Strand = Plus / Plus
```

```
Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
            ||||||||||||||||| |||||||| | |||||| |||| |||| |||| ||||||||| |
Sbjct: 117 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 176
```

```
Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
            ||||||||||||| |||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 177 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 236
```

```
Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
            || ||  |||| ||||||| |||| ||||| || ||||||| |||||||||| || |||
Sbjct: 237 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 296
```

```
Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
            ||  | |||  ||||| ||  ||||||||||||| ||||||||||||||| ||||| ||||
Sbjct: 297 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 356
```

```
Score = 58.0 bits (29), Expect = 1e-04
Identities = 53/61 (86%)
Strand = Plus / Plus
```

```
Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
            ||||||||| |||||||  || || |||||||| |||| |||||||||||||||||||||
Sbjct: 555 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 614
```

```
Query: 705 t 705
            |
Sbjct: 615 t 615
```

```
Score = 46.1 bits (23), Expect = 0.41
Identities = 35/39 (89%)
Strand = Plus / Plus


Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
           ||||||||||||| | || ||||||||| |||||||||||
Sbjct: 417 gaactgtcagtgatcgccaacttcagtgaacctgaaata 455
```

☐ >gi|4587839|gb|AF065897.1|AF065897 🅛🅤 Mus musculus strain A/J CD86 antigen (Cd8
          Length = 984

```
Score =  143 bits (72), Expect = 2e-30
Identities = 198/240 (82%)
Strand = Plus / Plus


Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
           |||||||||||||||||| ||||||| | ||||| |||| |||| |||| |||||||| |
Sbjct: 117 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 176


Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
           |||||||||||||| |||||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 177 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 236


Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
           || || |||| ||||||| |||| ||||| || ||||||| |||||||||||| || |||
Sbjct: 237 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 296


Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
           ||   | ||| ||||| || |||||||||||| |||||||||||||||| ||||| ||||
Sbjct: 297 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 356



Score = 58.0 bits (29), Expect = 1e-04
Identities = 53/61 (86%)
Strand = Plus / Plus


Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
           |||||||||| ||||||| || || ||||||| ||| |||||||||||||||||||||||
Sbjct: 555 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 614


Query: 705 t 705
           |
Sbjct: 615 t 615



Score = 46.1 bits (23), Expect = 0.41
Identities = 35/39 (89%)
```

Strand = Plus / Plus

```
Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
            |||||||||||||| | || ||||||||| |||||||||||
Sbjct: 417 gaactgtcagtgatcgccaacttcagtgaacctgaaata 455
```

☐ >gi|1127750|gb|U39462.1|MMB72G07 🄛 Mus musculus B7-2 gene, exon 7
          Length = 420

Score = 143 bits (72), Expect = 2e-30
Identities = 198/240 (82%)
Strand = Plus / Plus

```
Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
            ||||||||||||||||| ||||||| | ||||| |||| |||| |||| |||||||| |
Sbjct: 84  caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 143

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
            |||||||||||||| |||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 144 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 203

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
            || || |||| ||||||| |||| ||||| || ||||||||| |||||||||| || |||
Sbjct: 204 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 263

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
            || | ||| ||||| || |||||||||||| |||||||||||||||||| ||||| ||||
Sbjct: 264 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 323
```

☐ >gi|26348035|dbj|AK079513.1| 🄛🄤 Mus musculus 16 days neonate thymus cDNA, RIKEℕ
        enriched library, clone:A130091H03 product:CD86 antigen,
        full insert sequence
        Length = 2541

Score = 143 bits (72), Expect = 2e-30
Identities = 198/240 (82%)
Strand = Plus / Plus

```
Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
            ||||||||||||||||| ||||||| | ||||| |||| |||| |||| |||||||| |
Sbjct: 202 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 261

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
            |||||||||||||| |||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 262 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 321

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
```

```
                ||  ||  ||||  ||||||||  ||||  |||||   ||  ||||||||  ||||||||||| ||  |||
Sbjct:  322 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 381


Query:  381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat 440
                ||   | |||  |||||| ||  |||||||||||| ||||||||||||||| ||||| ||||
Sbjct:  382 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat 441



 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 53/61 (86%)
 Strand = Plus / Plus


Query:  645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
                |||||||||  |||||||  ||  ||   |||||||  |||  |||||||||||||||||||||
Sbjct:  640 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 699


Query:  705 t 705
                |
Sbjct:  700 t 700



 Score = 46.1 bits (23), Expect = 0.41
 Identities = 35/39 (89%)
 Strand = Plus / Plus


Query:  501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
                |||||||||||| | || |||||||||| |||||||||||
Sbjct:  502 gaactgtcagtgatcgccaacttcagtgaacctgaaata 540
```

☐ >gi|432478|gb|L25606.1|MUSB72X **L U G** Murine B7-2 mRNA, complete cds
          Length = 1183

 Score = 143 bits (72), Expect = 2e-30
 Identities = 198/240 (82%)
 Strand = Plus / Plus

```
Query:  201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
                |||||||||||||||||||| ||||||| | ||||| ||||  |||| |||| |||||||||  |
Sbjct:  183 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 242


Query:  261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
                |||||||||||||| ||||||||||||||||||||||| |||| ||||||||| | |||
Sbjct:  243 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 302


Query:  321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
                || ||  |||| |||||||| ||||  |||||  ||  ||||||||  ||||||||||| ||  |||
Sbjct:  303 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 362
```

```
Query: 381  gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat  440
             ||  |  |||  ||||| ||  ||||||||||| |||||||||||||||  ||||| ||||
Sbjct: 363  gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat  422
```

```
Score = 58.0 bits (29), Expect = 1e-04
Identities = 53/61 (86%)
Strand = Plus / Plus
```

```
Query: 645  aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg  704
             ||||||||||  ||||||| || ||  |||||||| ||| ||||||||||||||||||||||
Sbjct: 621  aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg  680
```

```
Query: 705  t  705
             |
Sbjct: 681  t  681
```

```
Score = 46.1 bits (23), Expect = 0.41
Identities = 35/39 (89%)
Strand = Plus / Plus
```

```
Query: 501  gaactgtcagtgcttgctaacttcagtcaacctgaaata  539
             ||||||||||||| | || |||||||||| ||||||||||
Sbjct: 483  gaactgtcagtgatcgccaacttcagtgaacctgaaata  521
```

>gi|546694|gb|S70108.1|S70108 [L] early T cell costimulatory molecule-1 [mice, 5C2
                 mRNA, 1115 nt]
          Length = 1115

```
Score =  143 bits (72), Expect = 2e-30
Identities = 198/240 (82%)
Strand = Plus / Plus
```

```
Query: 201  caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa  260
             ||||||||||||||||||  ||||||| | ||||| |||| |||| |||| ||||||||| |
Sbjct: 166  caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata  225
```

```
Query: 261  agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta  320
             ||||||||||||||| ||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 226  agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac  285
```

```
Query: 321  tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt  380
             || ||  |||| ||||||| |||| ||||| ||  || ||||||| ||||||||| || |||
Sbjct: 286  tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt  345
```

```
Query: 381  gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggcttgtat  440
             ||  |  |||  ||||| ||  ||||||||||| |||||||||||||||  ||||| ||||
Sbjct: 346  gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggctcgtat  405
```

```
 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 53/61 (86%)
 Strand = Plus / Plus


Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
           |||||||||| ||||||| || || ||||||| |||| ||||||||||||||||||||||||
Sbjct: 604 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 663


Query: 705 t 705
           |
Sbjct: 664 t 664



 Score = 46.1 bits (23), Expect = 0.41
 Identities = 35/39 (89%)
 Strand = Plus / Plus



Query: 501 gaactgtcagtgcttgctaacttcagtcaacctgaaata 539
           ||||||||||||| | || ||||||||| ||||||||||
Sbjct: 466 gaactgtcagtgatcgccaacttcagtgaacctgaaata 504



☐ >gi|15489434|gb|BC013807.1|  L U G  Mus musculus CD86 antigen, mRNA (cDNA clone M(
           IMAGE:4008635), complete cds
           Length = 2528

 Score =  141 bits (71), Expect = 9e-30
 Identities = 194/235 (82%)
 Strand = Plus / Plus


Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
           ||||||||||||||||| |||||||| | ||||| |||| |||| |||| ||||||||| |
Sbjct: 175 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 234


Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
           |||||||||||||| |||||||||||||||||||||||| |||| |||||||| | |||
Sbjct: 235 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 294


Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
           || || |||| ||||||| |||| ||||| || ||||||| ||||||||||| || |||
Sbjct: 295 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 354


Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggct 435
           ||  | ||| ||||| || ||||||||||| |||||||||||||||||| |||||
Sbjct: 355 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggct 409
```

Score = 58.0 bits (29), Expect = 1e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
           |||||||||| ||||||| || || ||||||| ||| |||||||||||||||||||||||||
Sbjct: 613 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 672

Query: 705 t 705
           |
Sbjct: 673 t 673

☐ >gi|31542363|ref|NM_019388.2| 🅛🅤·🅖 Mus musculus CD86 antigen (Cd86), mRNA
            Length = 2528

Score = 141 bits (71), Expect = 9e-30
Identities = 194/235 (82%)
Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
           |||||||||||||||| ||||||| | ||||| |||| |||| |||| |||| |||||||| |
Sbjct: 175 caagcttatttcaatgggactgcatatctgccgtgcccatttacaaaggctcaaaacata 234

Query: 261 agcctgagtgagctagtagtattttggcaggaccaggaaaacttggttctgaatgaggta 320
           ||||||||||||||| |||||||||||||||||||||| |||| ||||||||| | |||
Sbjct: 235 agcctgagtgagctggtagtattttggcaggaccagcaaaagttggttctgtacgagcac 294

Query: 321 tacttaggcaaagagaaatttgacagtgttcattccaagtatatgggccgcacaagtttt 380
           || |.| |||| ||||||| |||| ||||| || |||||||| ||||||||||| || |||
Sbjct: 295 tatttgggcacagagaaacttgatagtgtgaatgccaagtacctgggccgcacgagcttt 354

Query: 381 gattcggacagttggaccctgagacttcacaatcttcagatcaaggacaagggct 435
           || | ||| ||||| || |||||||||| |||||||||||||||||||| |||||
Sbjct: 355 gacaggaacaactggactctacgacttcacaatgttcagatcaaggacatgggct 409

Score = 58.0 bits (29), Expect = 1e-04
Identities = 53/61 (86%)
Strand = Plus / Plus

Query: 645 aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
           |||||||||| ||||||| || || ||||||| ||| |||||||||||||||||||||||||
Sbjct: 613 aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 672

Query: 705 t 705
           |
Sbjct: 673 t 673

☐ >gi|808027|gb|U17717.1|HSB72S3   Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ϵ
          Length = 484

 Score = 105 bits (53), Expect = 5e-19
 Identities = 53/53 (100%)
 Strand = Plus / Plus

Query: 130 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 182
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 260 gcactatgggactgagtaacattctctttgtgatggccttcctgctctctggt 312

☐ >gi|25188157|dbj|AB085744.1| Mesocricetus auratus mRNA for B7-2, complete cds
          Length = 2611

 Score = 101 bits (51), Expect = 8e-18
 Identities = 84/95 (88%)
 Strand = Plus / Plus

Query: 201 caagcttatttcaatgagactgcagacctgccatgccaatttgcaaactctcaaaaccaa 260
           |||||||||||||||| ||||||| ||||||||||||| |||| |||| |||||||| |
Sbjct: 183 caagcttatttcaataggactgcatacctgccatgcccatttacaaaggctcaaaataga 242

Query: 261 agcctgagtgagctagtagtattttggcaggacca 295
           ||||||||||||||| |||||||||||||||||||
Sbjct: 243 agcctgagtgagctggtagtattttggcaggacca 277

 Score = 56.0 bits (28), Expect = 4e-04
 Identities = 58/68 (85%)
 Strand = Plus / Plus

Query: 672 atgcagaaatctcaagataatgtcacagaactgtacgacgtttccatcagcttgtctgtt 731
           |||||||| ||| |||||| |||||||||||||||| | |||||||||| ||| ||||| ||
Sbjct: 654 atgcagatatcacaagacaatgtcacagaactgttcagcgtttccattagcctgtctatt 713

Query: 732 tcattccc 739
             ||||||
Sbjct: 714 ccattccc 721

 Score = 48.1 bits (24), Expect = 0.10
 Identities = 39/44 (88%)
 Strand = Plus / Plus

Query: 572 cataaatttgacctgctcatctatacacggttacccagaaccta 615
           ||||||||||||||||||||||||| | | |||||| ||| ||||||
Sbjct: 551 cataaatttgacctgctcatctaaagaaggttatccaaaaccta 594

```
Score = 48.1 bits (24), Expect = 0.10
Identities = 30/32 (93%)
Strand = Plus / Plus


Query: 403 gacttcacaatcttcagatcaaggacaagggc 434
            |||||||||||| |||||||||||||||| ||||
Sbjct: 385 gacttcacaatgttcagatcaaggacatgggc 416



Score = 44.1 bits (22), Expect = 1.6
Identities = 31/34 (91%)
Strand = Plus / Plus


Query: 507 tcagtgcttgctaacttcagtcaacctgaaatag 540
            |||||| | |||||||||||| ||||||||||||||
Sbjct: 489 tcagtgatggctaacttcagtgaacctgaaatag 522



□>gi|808031|gb|U17721.1|HSB72S7    Human CTLA-4 counter-receptor B7.2 (B7.2) gene, ɛ
           Length = 658

Score = 93.7 bits (47), Expect = 2e-15
Identities = 47/47 (100%)
Strand = Plus / Plus


Query: 963  ggaaccaacacaatggagagggaagagagtgaacagaccaagaaaag 1009
            |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 273  ggaaccaacacaatggagagggaagagagtgaacagaccaagaaaag 319



□>gi|3851167|gb|AF099105.1|AF099105    Homo sapiens B7.2 antigen (CD86) gene, promot
           Length = 1277

Score = 85.7 bits (43), Expect = 5e-13
Identities = 43/43 (100%)
Strand = Plus / Plus


Query: 1    ggaaggcttgcacagggtgaaagctttgcttctctgctgctgt 43
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1235 ggaaggcttgcacagggtgaaagctttgcttctctgctgctgt 1277



□>gi|44889504|gb|AY533858.1|   🅛🅤 Bos taurus CD86 mRNA, 3' UTR and partial cds
           Length = 2062

Score = 79.8 bits (40), Expect = 3e-11
Identities = 68/76 (89%), Gaps = 1/76 (1%)
Strand = Plus / Plus
```

```
Query: 1513 atcttgtgtacctgtgactaaacaactacctcctcagtctgggtgggacttatgta-ttt 1571
             ||||||| |||||||||||| |||||||||| ||||||||||||||| ||||||| |||
Sbjct: 686  atcttgtatacctgtgactgaacaactacctttcagtctgggtgggagttatgtatttt 745


Query: 1572 atgaccttatagtgtt 1587
             ||| ||||||||| ||||
Sbjct: 746  atggccttataatgtt 761



 Score = 69.9 bits (35), Expect = 3e-08
 Identities = 142/174 (81%), Gaps = 4/174 (2%)
 Strand = Plus / Plus


Query: 2054 agcaacagatggatagtctgtccaaatggacataagacagacagcagtttccctggtggt 2113
             ||||||||||||| |||||   |||||||||| |||| | |||||||||||||| ||  |||
Sbjct: 1231 agcaacagatggacagtctaaccaaatggacttaaggccgacagcagtttccttgcaggt 1290


Query: 2114 cagggagggggttttggtgatacccaagttattgggatgt--catcttcctggaagcagag 2171
             |||||||||||||| |||||| ||| || |||| |||| || |  ||||||||||||||
Sbjct: 1291 t-gggagggggttttgatgatagccagcttgttgtaatgtttcacccgactggaagcagag 1349


Query: 2172 ctggggagggagagccatcaccttgataatgggatgaatggaaggaggcttagg 2225
             ||||| ||||||||| |||| ||| |||| ||| || |||||||||||| ||||
Sbjct: 1350 ctgggaagggagagctatcatcttaataacgggtg-atggaaggaggcctagg 1402



 Score = 52.0 bits (26), Expect = 0.007
 Identities = 65/78 (83%)
 Strand = Plus / Plus


Query: 1662 taaggagttctcatccctctgtcagggtcagtaaggaaaacggtggcctagggtacaggc 1721
             ||||| |||||   ||||||||| |||||||||||||||||| | ||| | || || | | |
Sbjct: 823  taagggttctggtccctctgtgagggtcagtaaggaaagtgatggtccagtgtgctgac 882


Query: 1722 aacaatgagcagaccaac 1739
             ||||||||||||||||||
Sbjct: 883  aacaatgagcagaccaac 900



 Score = 52.0 bits (26), Expect = 0.007
 Identities = 107/134 (79%)
 Strand = Plus / Plus


Query: 985  aagagagtgaacagaccaagaaaagagaaaaaatccatatacctgaaagatctgatgaag 1044
             |||||||||||||||||   |||||||| | || |||   ||||||||||||||||||||||
Sbjct: 162  aagagagtgaacagactgcgaaaagagtagaactccaagaacctgaaagatctgatgaag 221


Query: 1045 cccagcgtgttttttaaaagttcgaagacatcttcatgcgacaaaagtgatacatgttttt 1104
```

```
                   |||| ||| | |||| | ||| |||||| | |||     ||||||| | |||| |||| |
Sbjct: 222   tccagtgtgatgttaacatttcaaagacagcctcagataacaaaagcgctacaaatttgt 281


Query: 1105 aattaaagagtaaa 1118
            |||||||||||||
Sbjct: 282  aattaaagagtaaa 295
```

☐ >gi|11464988|ref|NM_020081.1| **L U G** Rattus norvegicus CD86 antigen (Cd86), mRNA
Length = 942

Score = 73.8 bits (37), Expect = 2e-09
Identities = 115/141 (81%)
Strand = Plus / Plus

```
Query: 171  ctgctctctggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctg 230
            |||||||| | ||||| |||| |||||| ||||||||| ||||||   |||||| |||||
Sbjct: 70   ctgctctcagatgctgttcctgtgaagaggcaagcttacttcaatagcactgcatacctg 129


Query: 231  ccatgccaatttgcaaactctcaaaaccaaagcctgagtgagctagtagtattttggcag 290
            || |||| || |||| ||||||||| ||||| |||||||||| |||||||||||||||||
Sbjct: 130  ccgtgcccgttcacaaaggctcaaaacataagcccgagtgagctcgtagtattttggcag 189


Query: 291  gaccaggaaaacttggttctg 311
            |||| | ||||| | ||||||||
Sbjct: 190  gaccggaaaaagtcggttctg 210
```

Score = 60.0 bits (30), Expect = 3e-05
Identities = 36/38 (94%)
Strand = Plus / Plus

```
Query: 403  gacttcacaatcttcagatcaaggacaagggcttgtat 440
            |||||||||| |||||||||||||||| ||||||||||
Sbjct: 302  gacttcacaatgttcagatcaaggacacgggcttgtat 339
```

Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus

```
Query: 572  cataaatttgacctgctcatcta 594
            |||||||||||||||||||||||
Sbjct: 471  cataaatttgacctgctcatcta 493
```

☐ >gi|2627024|dbj|D50558.1| **L U G** Rattus norvegicus mRNA for membrane glycoprotein
Length = 942

```
Score = 73.8 bits (37), Expect = 2e-09
Identities = 115/141 (81%)
Strand = Plus / Plus


Query: 171  ctgctctctggtgctgctcctctgaagattcaagcttatttcaatgagactgcagacctg 230
            ||||||||| | |||||| |||| ||||||  ||||||||| ||||||  |||||| |||||
Sbjct: 70   ctgctctcagatgctgttcctgtgaagaggcaagcttacttcaatagcactgcatacctg 129


Query: 231  ccatgccaatttgcaaactctcaaaaccaaagcctgagtgagctagtagtatttttggcag 290
            || |||| || |||| |||||||| ||||| |||||||||||| ||||||||||||||||||
Sbjct: 130  ccgtgcccgttcacaaaggctcaaaacataagcccgagtgagctcgtagtattttggcag 189


Query: 291  gaccaggaaaaacttggttctg 311
            |||| | |||| | |||||||||
Sbjct: 190  gaccggaaaaagtcggttctg 210



Score = 60.0 bits (30), Expect = 3e-05
Identities = 36/38 (94%)
Strand = Plus / Plus


Query: 403  gacttcacaatcttcagatcaaggacaagggcttgtat 440
            |||||||||||| |||||||||||||||| ||||||||||
Sbjct: 302  gacttcacaatgttcagatcaaggacacgggcttgtat 339



Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus


Query: 572  cataaatttgacctgctcatcta 594
            |||||||||||||||||||||||
Sbjct: 471  cataaatttgacctgctcatcta 493
```

☐ >gi|940936|gb|U31330.1|RNU31330 L U Rattus norvegicus B7-2 mRNA, partial cds
            Length = 449

```
Score = 63.9 bits (32), Expect = 2e-06
Identities = 47/52 (90%)
Strand = Plus / Plus


Query: 260  aagcctgagtgagctagtagtattttggcaggaccaggaaaaacttggttctg 311
            |||||||||||||||||| ||||||||||||||||||| | |||| | |||||||
Sbjct: 5    aagcctgagtgagctcgtagtattttggcaggaccggaaaaagtcggttctg 56



Score = 60.0 bits (30), Expect = 3e-05
Identities = 36/38 (94%)
Strand = Plus / Plus
```

```
Query: 403  gacttcacaatcttcagatcaaggacaagggcttgtat 440
             |||||||||||| |||||||||||||||| ||||||||||
Sbjct: 148  gacttcacaatgttcagatcaaggacacgggcttgtat 185
```

```
 Score = 46.1 bits (23), Expect = 0.41
 Identities = 23/23 (100%)
 Strand = Plus / Plus
```

```
Query: 572  cataaatttgacctgctcatcta 594
             |||||||||||||||||||||||
Sbjct: 317  cataaatttgacctgctcatcta 339
```

```
 Score = 44.1 bits (22), Expect = 1.6
 Identities = 31/34 (91%)
 Strand = Plus / Plus
```

```
Query: 672  atgcagaaatctcaagataatgtcacagaactgt 705
             ||||||| ||| |||||| ||||||||||||||||
Sbjct: 411  atgcagatatcacaagacaatgtcacagaactgt 444
```

☐ >gi|1127751|gb|U39463.1|MMB72G08 **L** Mus musculus B7-2 gene, exon 8
          Length = 418

```
 Score = 58.0 bits (29), Expect = 1e-04
 Identities = 53/61 (86%)
 Strand = Plus / Plus
```

```
Query: 645  aattcaactatcgagtatgatggtattatgcagaaatctcaagataatgtcacagaactg 704
             ||||||||||  |||||||  || ||  |||||||  ||| |||||||||||||||||||||
Sbjct: 172  aattcaactaatgagtatggtgataacatgcagatatcacaagataatgtcacagaactg 231
```

```
Query: 705  t 705
            |
Sbjct: 232  t 232
```

☐ >gi|21217730|gb|AY095931.1| Meriones unguiculatus costimulatory molecule B7.2 mF
          cds
          Length = 1040

```
 Score = 50.1 bits (25), Expect = 0.026
 Identities = 49/57 (85%)
 Strand = Plus / Plus
```

```
Query: 261  agcctgagtgagctagtagtatttggcaggaccaggaaaacttggttctgaatgag 317
```

```
          |||||||| ||||||| || ||||| ||||||||||||| ||||   ||||||||| |||||
Sbjct: 145 agcctgagcgagctggtcgtattctggcaggaccagaaaaagctggttctgtatgag 201
```

☐ >gi|2338551|gb|AF013277.1|AF013277 🅄 Bombyx mori topoisomerase II (TOPOII) mRNA,
             Length = 6412

Score = 50.1 bits (25), Expect = 0.026
Identities = 25/25 (100%)
Strand = Plus / Minus

```
Query: 884  tattatatgtgtgatggttttctgt 908
            |||||||||||||||||||||||||
Sbjct: 2016 tattatatgtgtgatggttttctgt 1992
```

☐ >gi|26801335|gb|AC121585.3| 🅳 Mus musculus BAC clone RP23-265M4 from 5, complete
             Length = 195311

Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus

```
Query: 2233  actcctggctgagagaggaagag 2255
             |||||||||||||||||||||||
Sbjct: 59960 actcctggctgagagaggaagag 59982
```

☐ >gi|3790157|emb|AL022146.1|HS780M13 🅖🅳 Human DNA sequence from clone RP4-780M1:
             complete sequence
             Length = 78025

Score = 46.1 bits (23), Expect = 0.41
Identities = 23/23 (100%)
Strand = Plus / Plus

```
Query: 1002  aagaaaagagaaaaaatccatat 1024
             |||||||||||||||||||||||
Sbjct: 26005 aagaaaagagaaaaaatccatat 26027
```

Get selected sequences	Select all	Deselect all

Lambda   K   H
   1.37   0.711   1.31

Gapped
Lambda   K   H
   1.37   0.711   1.31

Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2280493
Number of Hits to DB: 34,755,694
Number of extensions: 2119444
Number of successful extensions: 12565
Number of sequences better than 10.0: 23
Number of HSP's better than 10.0 without gapping: 23
Number of HSP's gapped: 12561
Number of HSP's successfully gapped: 44
Number of extra gapped extensions for HSPs above 10.0: 12497
Length of query: 2781
Length of database: 11,051,402,435
Length adjustment: 23
Effective length of query: 2758
Effective length of database: 10,998,951,096
Effective search space: 30335107122768
Effective search space used: 30335107122768
A: 0
X1: 11 (21.8 bits)
X2: 15 (30.0 bits)
X3: 25 (50.0 bits)
S1: 12 (25.0 bits)
S2: 21 (42.1 bits)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Bennett et al.	) I hereby certify that this paper is being
	) deposited with the United States Postal
Serial No.: 10/444,206	) Service as Express Mail, Airbill No.
	) EV233430269US, in an envelope addressed
Filed: May 23, 2003	) to: Mail Stop Conversion, Commissioner for
	) Patents, P.O. Box 1450, Alexandria, VA
For: Oligonucleotide Compositions	) 22313-1450 on March 9, 2004
and Methods for the Modulation of	)
the Expression of B7 Protein	)
	)
Group Art Unit: 1635	)
	)
Examiner: To be Assigned	) _____
	) Laura Frasher

REQUEST FOR CONVERSION OF NONPROVISIONAL APPLICATION TO A PROVISIONAL APPLICATION PURSUANT TO 37 C.F.R. 1.53(C)(2)

Mail Stop Conversion
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

   The Applicants hereby request that U.S. Application Serial No. 10/444,206 be converted to a U.S. Provisional Patent Application pursuant to 37 C.F.R. 1.53(c)(2). The Applicants submit herewith the fee for this request under 1.17(q). The Commissioner is hereby authorized to charge any additional fees which may be required to Deposit Account No. 13-2855. A duplicate of this paper is enclosed.

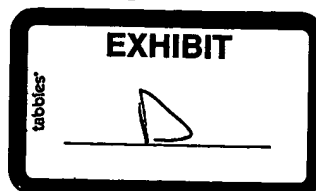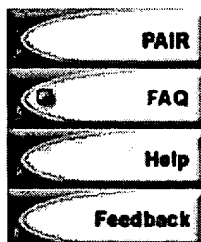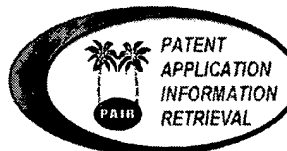   Respectfully submitted,

         MARSHALL, GERSTEIN & BORUN LLP
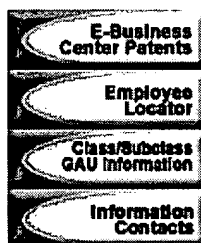
By _____

March 9, 2004
         Joseph A. Williams, Jr. (Reg. No. 38,659)
         6300 Sears Tower
         233 South Wacker Drive
         Chicago, Illinois 60606-6357
         (312) 474-6300

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Search results for application number:10/444,206			
Application Number:	10/444,206	Customer Number:	-
Filing or 371(c) Date:	05-23-2003	Status:	Docketed New Case - for Examination
Application Type:	Utility	Status Date:	04-20-2004
Examiner Name:	EPPS FORD, JANET L	Location:	ELECTRONIC
Group Art Unit:	1635	Location Date:	-
Confirmation Number:	5228	Earliest Publication No:	US 2004-0023917 A1
Attorney Docket Number:	30566/39365	Earliest Publication Date:	02-05-2004
Class/ Sub-Class:	514/044	Patent Number:	-
First Named Inventor:	C. Bennett, Carlsbad, CA (US)	Issue Date of Patent:	-
Title Of Invention:	Oligonucleotide compositions and methods for the modulatio expression of B7 protein		

Select Search Option

Assignments
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Published Documents

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File History	
Date	Contents Description
04-29-2004	Correspondence Address Change
09-29-2003	New or Additional Drawing Filed
04-20-2004	IFW TSS Processing by Tech Center Complete
08-18-2003	Preliminary Amendment
04-20-2004	Case Docketed to Examiner in GAU
10-08-2003	Application Dispatched from OIPE
10-09-2003	Application Is Now Complete
09-24-2003	Additional Application Filing Fees
09-24-2003	A statement by one or more inventors satisfying the requirement ur 115, Oath of the Applic
09-24-2003	Applicant has submitted new drawings to correct Corrected Papers
07-24-2003	Notice Mailed--Application Incomplete--Filing Date Assigned
06-13-2003	CRF Is Good Technically / Entered into Database
06-11-2003	Cleared by OIPE CSR
06-11-2003	Cleared by OIPE CSR

06-06-2003	IFW Scan & PACR Auto Security Review
06-04-2003	IFW Scan & PACR Auto Security Review
05-23-2003	CRF Disk Has Been Received by Preexam / Group / PCT
05-23-2003	Initial Exam Team nn

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